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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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37.2	37.2	37.5	38.1	38.1	38.4	38.9	39.7	40.5	64.3	77.6	77.6	82.6	91.1	91.4	92.6	94.5	97.3	100.0	Query	*
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AY085713	BT012975	CAANN	AR231102	BD236034	BD236006	AF006197	GHU73746	GHU89609	AY356355	AF332435	CQ806050	F14D7	ATU28415	ATANNEX	BT003359	AY086570	AY072347	AF083913	ID	
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## ALIGNMENTS

AF083913 LOCUS DEFINITION ACCESSION VERSION	AF083913 1230 bp mRNA linear PLN 02-JUN-1999 Arabidopsis thaliana annexin (AnnAtl) mRNA, complete cds. AF083913 AF083913.1 GI:4959105
SOURCE ORGANISM	Arabidopsis thaliana (thale cress)  Arabidopsis thaliana (thale cress)  This control of the cress of the cress of the control of the cress of the cr
	Bukaryota, Viridiplantae, Streptophyta, Embaryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, endicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
REFERENCE AUTHORS	1 (bases 1 to 1230) Clark,G.B. and Roux,S.J.
TITLE	Isolation and Characterization of Two Different Arabidopsis Annexin CDNAs (Accession Nos. AF083913 and AF083914) (PGR 99-065)
JOURNAL	CUNAS (ACCESSION NOS. AFUBJYIJ ANG AFUBJYI4) (PGK 99-U65) Plant Physiol. 120 (1), 340 (1999)
REFERENCE	2 (bases 1 to 1230)
TITLE	Clark, G.B. and koux, S.J. Direct Submission
JOURNAL	Submitted (12-AUG-1998) Botany, University of Texas, 24th at
FEATURES	Location/Qualifiers
source	11230
	organism="Arabidopsis thaliana" /mol_type="mRNA"
	/cultivar="Columbia" /db xref="taxon:3702"
gene	11230
CDS	/gene="AnnAt1" 34987
	/gene="AnnAt1" /note="calcium-binding protein"
	<pre>/codon start=1 /product="annexin"</pre>
	/protein_id="AAD34236.1"
	<pre>/db_xref="GI:4959106" /translation="MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAE</pre>
	QRKVIRQAYHETYGEDLLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSS NOVIMEVACTRTSTOLIHAROAYHARYKKSIFEDVAHHTTGDFRKLLVSLVTSYRYEG
	DEVNMTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILK
	SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID

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GCACTTCTCGGTGAAGATGATGCTTAATCAATCCACTCCACAGAGAAACATAAGCTGC
                                                                       ATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTC
                                                                                                          ACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGAGTACCAGCGCAGGAACAGC
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                                              ATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTC
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                                                                                                                                                                                                                                                                                                                                                 collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submission
Submitted (02-JAN-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nguyen,M., Karlin.Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1208)
Trachia Maranda M.
                                                                                                                                                                               Nguyen, M, (SSP/Stanford) and Seki, M. equally to this work. Shinozaki, K. (SSP/Stanford) contributed equally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana Ca2+-dependent mem annexin (At1g35720) mRNA, complete cds. AY072347
                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Genomic Sciences Center (GSC) members carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                         e-mail for correspondence: arab@sequence.stanford.edu
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                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                              (SSP/Stanford) and Seki, M.
                                                                                                       db_xref="taxon:3702"
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Query Match
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                                                                                  TTGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGT
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Pred. No. 1.5e-292;
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FEATURES	COMMENT	JOURNAL REFERENCE AUTHORS TITLE TOTRNAL	MEDLINE PUBMED REFERENCE AUTHORS TITLE	AUTHORS TITLE JOURNAL	REFERENCE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM		114	15	Oy 109	Oy 103 Db 102	Οy 97 Db 96		<b>10</b>	Qy 850
this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or LAGY contain polymorphisms when compared to sequences from Col-0. Genset carried out the library production and sequencing of the 5' sequences, selection of clones, and sequence assembly.	Audititied (11 MAR 2002) CEIEB, 1110, 3000 Malibu, CA 90265, USA Malibu, CA 90265, USA This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of	Unpublished  (Dases 1 to 1192)  Tobases 1 to 1192)  Brover, V., Troukhan, M., Alexandrov, N., Lu, YP., Flavell, R. and Feldmann, K.  Direct Submission  Submitted (11-MAR-2002) Cores Toc 3007 Malibu Canvon Road	<pre>22088475 1209376 1209376 2 (bases 1 to 1192) Brover,V., Troukhan,M., Alexandrov,N., Lu,YP., Flavell,R. and Feldmann,K. Feldmann,K. Feldmann,K.</pre>	Haas, B.J., Volfovsky, N., Town, C.D., Trouknan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome annotation and the sequences greatly improve genome annotation.	acheo cots; psis.	•	AY086570 1192 bp mRNA linear PLN 14-APR-2003 Arabidopsis thaliana clone 25846 mRNA, complete sequence.	9 GAGAGACAGAGAGAACCAGTGTGGTCTCTTAAGTTATATATA	0	O TICTACAAAAACCITGITTGITTCTGITGGGTGTGTTTTGAGTTCCTAAATAATGCAAAAGA 1149 	O TCTGTTATCTCCTTCTCCCTCTCTCTTTGATGAGTTTCAAATCGTTTGATTTGT 1089	O GGTGAAGATGATGCTTAATCAATCAATCCTCCACAGAGAAACATAAGCTGCTCTACAGCT 1029 		GAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTC S	0 GCTGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTG 909

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/db_xref="taxon:3702"
/clone="55846"
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/protein_id="RAM63633.1"
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SLEEGDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
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Pred. No. 1.1e-283;
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RESULT 4 BT003359 LOCUS ACCESSION VERSION KEYWORDS COMMENT SOURCE ORGANISM REFERENCE DEFINITION TITLE JOURNAL AUTHORS Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T., Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinn, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission

Submitted (29-JAN-2003) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1139) BT003359 1139 bp mRNA linear E Arabidopsis thaliana Ca2+-dependent membrane-binding annexin (At1g35720) mRNA, complete cds. Arabidopsis thaliana (thale Arabidopsis thaliana BT003359.1 FLI\_CDNA. e-mail for correspondence: arab@sequence.stanford.edu GI:28059005 cress) PLN 29-JAN-2003 protein

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Tripp, M., Southwick, A., Palm, C.J., Jones, T., Wu, T., Chen, H., Cheuk, R., Southwick, A., Palm, C.J., Jones, T., Wu, T., Chen, H., Chand, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Nguyen,M., Tripp,M., Southwick,A., Palm,C.J., Jones,T., Wu,T., Chen,H., Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Kim,C.J., Quach,H.L., Onodera,C.S., Shinn,P., Tang,C.C., Toroumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.

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Best Local Similarity
Matches 1139; Conser
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      ATCAATGCTACTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
                                                                                                GATGAAGTGAACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
                                                                                                                   GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
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                                   GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                                                    GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
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ilarity 100.0%;
Conservative
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DEVNMTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILK
SLEEGDDDDKFLALLRSTIQCLTRFELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ecotype="Columbia"
/note="This clone is in
PCR product using RIKEN
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/chromosome="1"
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AUTHORS
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X99224.1 GI:1429206
annexin; calcium binding p
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                  Submitted (09-JUL-1996) R. Schantz, Institut de Moleculaire des Plantes, CNRS, 12 Rue de General Strasbourg, FRANCE
                                                                                                                                                                                                                                                                                                                                                                Schantz, R.,
                                                                                                                                                                                                                                         Related
                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                              Unpublished
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/codon_start=3
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                                                                              function="calcium
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/translation="ILKVSDSVPAPSDDAEQLETAPEGWGTNEDLIISILAHRSAEQR
KVIRQAYHETYGEDLLKTLDKELSNDFERAILLWTLEPGERDALLANBAYKRWTSSNQ
VLMEVACTRTSTQLLHARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDE
VMMTLAKQEAKLVHEKIKOKHYNDEDVIRILSTISKAQINATPRRYQDDHGEBIIKSL
EEGDDDDKFLALLRSTIGCLTRFELFYYDVLABAINKTGTDEGALTRIVTTRABIIDLK
VIGEEYQRRNSIPLRAITKONCGDYGKMLVAIFGEDDA"
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Kush, A. K.

Direct Submission

Direct Submission

Direct Submission

Submitted (06-JUN-1995) Anil K. Kush, Institute of Particle Control Control
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Gidrol, X., Sabelli, P.A., Fern, Y.S. and Kush, A.K.
Annexin-like protein from Arabidopsis thaliana reso
mutant of Escherichia coli from HZO2 stress
Proc. Natl. Acad. Sci. U.S.A. 93 (20), 11268-11273
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Query Match
Best Local Similarity
Matches 1149; Conserv

Conservative

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91.1%;

Score 1120; Pred. No. 6. Mismatches

.4e-273; DB

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Length 1159; Indels

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-JUN-2000) Plant Gene Expression Center, 800 Buchanan St., Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced gi:6693723.
The sequence is of BAC F14D7 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 6954 by because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of complete seq AC021198
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Liu,S.X., Chan,A., Sakano,H., Yu,G., Lee,J.M., Lenz,C., Pham,P., Toriumi,M., Chin,C., Chiou,J., Choi,E., Chang,M., Gonzalez,A., Howng,B., Liu,A., Vaysberg,M., Altafi,H., Brooke,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Hansen,N.F., Johnson-Hopson,C., Klan,S., Kim,C., Lam,B., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R., Federspiel,N.A., Theologis,A. and Yu,G.

Theologis,A. and Yu,G.

The sequence of BAC F14D7 from Arabidopsis thaliana chromosome 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Street, Albany, CA 94710, 4 (bases 1 to 81513)
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Submitted (15-JAN-2000) Pl
Street, Albany, CA 94710,
3 (bases 1 to 81513)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-FEB-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/gene="F14D7.1"
join(1553. .4628,4713. .4999)
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/note="Contains similarity to receptor protein kinase-like
/note="Contains a eukaryotic protein kinase domain pF|00069. EST
gb|AI997574 comes from this gene."
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                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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                                                                                                                                                          L553. .4999
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                                                                                                                                                                                                                     db_xref="taxon:3702"
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0, USA
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0, USA
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misc_feature
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LSQNKLTGS I PSSLGNLKNLTLLSJFQNYLTGG I PPKCHT ESMI DLELSNNKLTGSI
PSSLGNLKNLT ILLYLENYLTGVI PPELGNMESM IDLELSNNKLTGSI
PSSLGNLKNLT ILLYLENYLTGVI PPELGNMESM IDLQLNNNKLTGS I PSSFGNLKNL
TYLYLYLNYLTGVI PQELGNMESM INLDLSQNKLTGG VPDS FGNFTKLESLYLRVNHL
SGA I PPGVANGSHLTTLLLDTNNFTGFF PETVCKGRKLQNISLDYNHLEGGP I PKSLRD
CKSLI RARFLGNKFTGDI FEAFGI Y PDLINFID PSHNKFHGEI SUMEKS PKLGALI MS
NNN I TGA I PTELMNMTQLVELDLSTNNLEGELPEAIGNLTNLSRLRLNGNQLSGRVPA
GLS FILTNLESLDLSSNNFSSE I PQTFDSPLKLHDMNLSBUKFTOGS I PRLSKLTQLTQL
DLSHNQLDGEI PSQLSSLQSLDKLDLSHNNLSGLI PTT PEGMI ALTNVD I SNNKLEGP
LPDTPTFRKATADALEENI GLCSNI FKQRLKPCRELKKPKKNGNLVWIL LVFILGYLV
ILS I CANTFTY CIRKRKLQNGRNTD PETGENMS I FSVDGKFKYQDI I ESTNEFD PTHL
I GTGGYSKVYRANLQDTI I AVRALHDT I DEEI SKEVVKQBFLNEVKQALALTSI RHRNVVK
LFGFCSHRRHTPLI YEYMEKGSLINKLLANDEBARATTWTKK INVVKGVAHALS YMHDD
RITP I VHRDI SSGNI ILLDNYTAKI SDFGTAKLLKTDSSNWSAVAGTYGYVAPEFAYT
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DEVNNTLAKQEAKLVHEKIKOKHYNDEDVIRILSTRSKAQINATTNRYQDDHGEELK
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LKVIGESYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"

complement (7937...1730)

/gene="F14D7.3"...
                                                                 ANYVIQTALSVTKGPVRAKLVAKVYRYGKLHSSPYCKKIFSKTILKK"
12116. .14526
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gb AL161513
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join(5917. .599:
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NLAYVDLSMNLLSGTIPPQFGNLSKLIYFDLSTNHLTGEISPSLGNLKNLTVLYLYLHQN
YLTSVIPSELGNMESMTDLALSQNKLTGSIPSSLGNLKNLMVLYLYENYLTGVIPPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Contains similarity to a putative protein CAB78009
gi|7267527 from Arabidopsis thaliana BAC T32A17
gb|AL161513. It contains Pumilio-family RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Identical to annexin (AnnAt1) mRNA from Arabidopsis
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note="Contains similarity to Tal-1_transposon gb|X13291"
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NLMARDQIGCRALQKLVEEGITVLDSKVIFLEIIDHVVELSMDFLGNYIVQKLLVVSDE
EQRTMIVSVLTSKPRELIKICLNTNGTRVIQKMIKTVKTVGQILALVKSALEFGFLVLV
NDSNGYHVLQSCLSFLIKICLNTNGTRVICKHLLISFLFLTYUSSDECCEIWCGTVUQCLI
DQQVSSVNLLLAFFRTHCIELATQKFSSHVIEKCLRKYPESABIYRELLSYFNFEQLL
DQQVSSVNLLLAFFRTHCIELATQKFSSHVIEKCLRKYPESABIYRELLSYFNFEQLL
DQQVSSVNLLLAFFRTHCIELATQKFSSHVIEKCLRKYPESABIYRELLSYFNFEQLL
                                                                       DKYMNSAETRAVWGTALTRMLLRNISAHILSPITYLIYATIYLIQVTVMDWQPWERTTA
WAYRKAMTNETLMGGGAGTSGVPLTDTEPDSIPIS KGGEKVTDDDBERERDRLEFMWRT
QQQEERWRENGATQNGTLAGATQIDATWGDTGGTRARALNFGGGDIFKGNPREDLOLTLA
RAETQEVCTQVVALSSSDSTFGMPTSLSTSVSFSSDDLMDVTDSSNNNSSSCIDKGKG
IMIDERITTKEIGAGSTNTRVSEVLRNELMVKDTPVFTVLYDRDAPPVFDDPEKEDAL
HRALKYADNBSDDIYIGEIFKKSEDCATKLAHLAHWKFHFIYAKSGFNIVANVCVSD
TCPWRVYATKLPDSDWFEVRSTTQTHTCSVDARGDFHKQASTVVIGKLMRTKXIGVGR
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/gene="F14D7.6"

join(44612. .44780, 45014. .45403,45501. .45644,45676. .46134,

join(44612. .44780, 45014. .45403, 45501. .45644,45676. .46134,

46297. .46476,46633. .47029,47113. .47505,47737. .48082,

48145. .48411,48465. .48541,48632. .48698)

/gene="F14D7.6"
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/gene="F14D7.5"
/note="Contains similarity to a putative RNA-binding /note="Contains gi|6587864 from Arabidopsis thaliana T1II1 gb|Ac012680. It contains Pumilio-family RNA binding domains PF|00806."
GPRANELRRMLRQDYALIQPYFKCLLETNPNSLVAMETEKDNSGVERFKYLFFALDAC
VQGYAYMRKVIVIDGTHLRGRYGGCLVAASAQDANFQVFPIAFGIVNSKNDEAWTWFM
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/gene="F14D7.5"
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                                                                                                                                                                                                                                                                                                                                                           /translation="mSDIYGVARYHLYTLVYLLAVYSLLCIKEKPTRLKTLVSDKINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb AC005561."
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GLSSHPTISNIAANLFCEEGLIGCSSTSTSFKLSLLKHKAFTLEKVDADDEKHKKNED
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23655. .23686))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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/protein_id="AAF79884.1"
/db_xref="GI:8778969"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Strong similarity to a mutator-like transposase
yi|4063759 from Arabidopsis thaliana BAC T14A4
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 TTTCGCAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCACAGAAGTGC
                     TTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCACAGAAGTGC
                                                      82.6%;
92.2%;
                                Pred. NC.
O: Mismatches
                                                      Score 1016.2;
Pred. No. 1.1
                                                         1.1e-246;
                                                                  DB 8;
                                                                  Length
                                                                   81513;
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 GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
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Inze,D., de Veylder,L. and Vlieghe,K.
Identification of novel e2f target genes and
Patent: WO 2004055798-A 2461 29-APR-2004;
CropDesign N.V (BE)
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Arabidopsis thaliana
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                    Submitted (28-DEC-2000) Plant Gene Expression Center, 800 Buchanas Street, Albany, CA 94710, USA 3 (bases 1 to 954)
Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
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Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L.,
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R.,
Jones, T., Kim, C.J., Nguyen, M., Palm, C.J.R., Southwick, A.,
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R., and Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Erassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       Yamada, K., Liu,S.K., Sakano,H., Pham,P.K., Banh,J., Etgu,F
Yamada,K., Liu,S.K., Sakano,H., Pham,P.K., Banh,J., Etgu,F
Lee,J.M., Toriumi,M., Yu,G., Brooke,S., Chao,Q., Chen,H.,
Karlin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
Falm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R.
                                                                                                                                        Submitted (07-MAY-2003) Plant Gene
Street, Albany, CA 94710, USA
Annotation based on July 2002 versi
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FLI CNNA.
Arabidopsis thaliana (thale cress)
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Arabidopsis thaliana clone C00123
membrane-binding protein annexin (
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                                                                                                                                                                                                       Submission
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                organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                            to Genbank.
                                                                                                  ocation/Qualifiers
                                                                                                                                            version
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(e) putative Ca2+-dependent
(At1g35720) mRNA, complete co
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len, H.,
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GAGGAAGGAGATGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTGCTTG
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                                                                                    ATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
                                                                                                                                                                  GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                          GCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCAC
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                                                             ATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
                                                                                                                                            GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                                                                                                                                                                                                                            GATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
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/ecotype="Columbia"
/note="This clone is now in pUNI 51 vector. Previous1:
it was in pUNI-T3-D/V5-His-TOPO under the clone number
C00123."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAG48798.1"
/db_xref="G1:12083278"
/db_xref="G1:12083278"
/translation="MARTKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAE
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ORKVIRQAYHETYGEDLLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSS
NQVLMEVACTRYSTQLLHARQAYHARYKKSLEEDVAHTTTGDERKLLVSILVTSYRYEK
DEVNMYLAKORAKLYHEKIKOKHYNDEDVIRILSTRSKAQINATENRYKDDHGEELK
SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
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/product="putative Ca2+-dependent
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0; Mismatches
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420 453 360 393 300 333

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Brassica juncea
Brassica juncea
Brassica juncea
Brassica juncea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Brassicaceae;
rosids; eurosids, I; Brassicales; Brassicaceae; Brassica.
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Brassica jun
AY356355
AY356355.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jami,S.K. and Kirti,P.B.
Direct Submission
Submitted (30-JUL-2003) Department of Plant Sciences, School of Life Sciences, University of Hyderabad, Gachibowli, Hyderabad, Andhra Pradesh 500046, India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rosids; eurocally 1 (bases 1 to 954)
1 (bases 1 to 954)
Jami, S.K. and Kirti, P.
Jami, S.K. and From the
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 AGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGAAGAC
                                                   AGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCAC
                                                                                             ATGGCGACTCTTAAGGTTTCTTCTTCTGTTCCTTCTCCCTCTGAAGATGCTGAGCAATTG
                                                                                                                  ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTTCTGATGATGCTGAACAATTG
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                                AAAAGCGCATTTGATGGATGGGGTACCAACGAGGAATTGATCATATCAATCTTGGCTCAC
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                                                                                                                                                              64.3%;
llarity 89.3%;
Conservative
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SLEEGDEDDKFLGLLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVATRAEID
LKVIGQEYQRRNSIPLEKAITKDTRGDYEKMLIALLGEDDA"
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Brassica juncea"
/mol_type="mRNA"
/db_xref="taxon:3707"
/tissue_type="floral bud"
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                                          Gossypium hirsutum (upland cotton)
Gossypium hirsutum
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

1 (bases 1 to 1141)
Shin, H. and Brown, R. M. Jr.
             Direct Submission
Submitted (13-FEB-1997)
                                                                                                                                                                                             GHU89609
Gossypium hirsutum fiber
U89609
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 GAAATGACATAAACAAGGACTT--
                       GCGAGGAAATTCTCAAGAGTCTTGAGGAAGGAAGGATGATGACAAGTTCCTTGCACTTT
                                                                                                                        AGCTGGTCCATGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCT
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/protein_id="AAC33305.1"
/db_xref="GI:3493172"
/db_xref="GI:3493172"
/translation="MATLTVPTTVPSVSEDCEQLRKAFSGWGTNEGLIIDILGHRNAE
/translation="MATLTVPTTVPSVSEDCEQLRKAFSGWGTNEGLIIDILGHRNAE
QRULIRKTYAETYGEDLKALLDKELSNOFERLVLLWALDPAEROALLAWSATKRWTSS
RQVLMEIACTRSANQLLHARQAYHARYKKSLEEDVAHHTTGDFRKLLLPLVSSYRYEG
EEVNMNLAKTEAKLLHEKISDKAYSDDDVIRLATRSKQINATLMYKNEYGNDINK
DIKADPKDEFLALLRSYFYKCLVYPEKYPEKYLALIAINRRGTDEGALTRVVCTRAEVDL
KIIADEYQRRNSVPLTRAIVKDTHGDYEKLLLVLAGHVEN"
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2 (bases 1 to 948)
Potikha,T.S. and Delmer,D.P.
Direct Submission
Submitted (09-OCT-1996) Plant Sciences, Hebrew 1
Ram Campus, Jerusalem 91904, Israel
On Aug 20, 2001 this sequence version replaced
Location/Qualifiers
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Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; endicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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Delmer, D.P. and Potikha, T.S.
Structures and functions of annexins
Cell. Mol. Life Sci. 53 (6), 546-553
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/protein_id="AnB87993.2"
/brotein_id="AnB87993.2"
/db_xref="GI:15214410"
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RNLIRKTYAETYGEDLLKALDKELSNDFERLVLLWALDPAERDALLANEATKRWTSSN
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CVLMEIACTREANQLLHARQAYHARYKKSLEEDVAHTTTGDFHKLLLDLVSSYRYEGE
                                                                                                                                                                                /gene="AnnGh1"
/function="evidence suggests that annexins may bind to influence activity of callose synthase"
/note="contains 4 repeats characteristic of other annexins; shows evidence of conserved calcium-binding domains; by comparison with other plant annexins as we as with the size of native cotton fiber annexin, this clone probably lacks 5'coding sequence for only the N-terminal Met; calcium binding protein"
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Lavatera thuringiaca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Lavatera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-MAY-1997) Biological Sciences, Universite du Quebec, Montreal, C.P. 8888, Succ. Centre-Ville, Montreal, Quebec H3C 3P8,
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Vazquez-Tello, A. and Uozumi,
Direct Submission
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Breton,G., Vazquez-Tello,A., Danyluk,J.
Two novel intrinsic annexins accumulate
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Vazquez-Tello, A. and Uozumi, T.
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Materials and method for
polysaccharides.
BD236006
BD236006.1 GI:33045776
JP 2002527055-A/28.
1 (bases 1 to 2588)
Bloksberg, L.N.
Materials and method for modification of plant cell Patent: JP 200257056-A 28 27-AUG-2002;
GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER
                                                      Eucalyptus grandis
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
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Location/Qualifiers
1. .2588
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/db_xref="taxon:71139"
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FORESTS LTD

OS Eucalyptus grandis (flooded gum)

PN JP 2002527056-A/28

PD 27-AUG-2002

PF 08-OCT-1999 JP 2000575985

PR 13-OCT-1998 US 09/170862,11-AUG-1999 US 60/

LEONARD NATHAN BLOKSBERG

PC C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/12,C12

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OCC Materials and method for modification of plant ce
                                                      Materials and method for modification polysaccharides
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Eucalyptus
grandis
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Score 471.8; DB 6; Pred. No. 1.4e-108; 0; Mismatches 302; Length 2588; ω •-

AAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCA AGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTT TCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGA GGACCTCCTCAAGGCATTGGACAGAGAACTTACCAATGATTTCGAGAGGCTGGTGGTCCT TCATAGGAATGCGGCGCAGAGGAAGCTGATTCGGCAAACCTATGCCGAGACTTACGGCGA AACAATGTCGACTCTCACCGTCCCGCAGCCACTGCCCCCTGTAGCCGATGACTGCGAGCA 1565 1505 149 1445 1625 269 209

GACTTCAAGCAACCAAGTTCTTATGGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCT TTGGTCACTTGATCCGGCTGAACGTGATGCGTACTTGGCGAATGAAGCGACGAAAAGATG GTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTACAAAAAAGATG GACTTCAAGCAACCAGGTTCTAATGGAAATAGCCTGCACGAGGTCTCCGCAGCAGTTGCT 449 1745 389 1685 329

CCACACTACCGGTGACTTCAGAAAGCTTTTTGGTTTCTCTTGTTACCTCATACAGGTACGA CCACACAACTGGAGATTTTCGTAAGTTGCTGGTACCTCTTGTGAGCTCCTACCGTTATGA 1865 1805

1925 569

CGA 209	150 TCACAGAAGTGCTGAACAGAGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGA	8
GGC 149    GGG 210	90 ATTGAGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCATTTGGC 	B 8
GCA 89     GCA 150	30 AAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCA	B 8
ps 1;	ery Match 38.1%; Score 468.6; DB 6; Length 1293; St Local Similarity 68.4%; Pred. No. 9.6e-108; Caps 664; Conservative 0; Mismatches 304; Indels 3; Gaps	Query Ma Best Loc Matches
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/00,C12N5/	27-AUG-2002 27-AUG-2002 08-OCT-1999 JP 2000575985 13-OCT-1998 US 09/170862,11-AUG-1999 US 60/148 DNARD NATHAN BLOKSBERG C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/12,C12N15	
	FORESTS LTD OS Pinus radiata (radiata pine) ON TD 2002577656 /66	COMMENT
GE -	Bloksberg, L.N. Materials and m Patent: JP 2002 GENESIS RESEARC	AUTHORS TITLE JOURNAL
Tracheophyta; Pinus; Pinus.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 1293)	REFEREN
	BD236034 GI: BD236034.1 GI: BD236034.1 GI: JP 2002527056-F Pinus radiata	ACCESSION VERSION KEYWORDS SOURCE ORGANISM
.JUL-2003	BD236034 1293 bp DNA linear PAT 17- Materials and method for modification of plant cell wall	RESULT 15 BD236034 LOCUS DEFINITION
	2343 TACAAGTACTC 2353	₽
	990 AATCAATCCTC 1000	Ş
ATC 989    ATT 2342	930 CACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTCGGTGAAGATGATGCTTAATC	유 성
AGA 929     GGA 2282	870 CATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGA	용 성
GGT 869 	810 AACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGT	<u> </u>
TGG 809	750 CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAACTGG	B 8

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Search completed: August 22, 2005, 09:01:37
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Aaa67128 Pinus rad
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## ALIGNMENTS

Arabidopsis thaliana DNA fragment SEQ ID NO: 6580

17-OCT-2000 (first entry)

AAC34418;

AAC34418 standard; DNA; 1192 BP.

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Query Match
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                                                   AAGCTGGTCCATGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATC
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99.1%;
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Pred. No. 1.2e-286;
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Query Match 93.1%;
Best Local Similarity 98.1%;
Matches 1171; Conservative
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                                  CAAAACTGGAACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGA
                                                                                                      TCTCAAGAGTCTTGAGGAAGGAGATGATGATGACAAGTTCCTTGCACCTTTTGAGGTCAAC
                                                                                                                                         TGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAG
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                                                                    CATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAA
                                                                              CATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAA
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99US-0161993P.
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Pred. No. 3.7e-282;
0; Mismatches 17;
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                                             The invention relates to novel isolated lipid metabolism proteins (LMP) and encoding nucleic acids comprising a polynucleotide sequence encoding a polypeptide that functions as a modulator of seed storage compounds in a plant. The LMP nucleic acid is useful in producing transgenic plants with increased levels of seed storage compound, e.g. lipid, a fatty acid, a starch or a seed storage protein, as markers for specific regions of the genome and for evolutionary and protein structural studies. The present sequence represents an LMP nucleic acid of the invention.
                                                                                                                                                                                                                                                                                                                             New lipid metabolism proteins and nucleic acids, useful in producing transgenic plants with increased levels of seed storage compound, e. lipid, a fatty acid, a starch or a seed storage protein.
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Query Match Best Local Similarity Matches 954; Conserv

100.0%; \*\*

Score 954; DB; Pred. No. 2e-0; Mismatches

DB 12; 2e-233;

Length

954; 0

Indels

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WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                            gene; ss; plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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                                                                                                                                                                                                                  18-OCT-2002; 2002EP-00079408
                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                    Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2461.
                                                                                                                                                                                                                              20-OCT-2003; 2003WO-EP011658
                                                                                                                                                                         2004-348466/32.
DB; ADN74567.
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up component of the component of Altering plant characteristics, useful for producing plants for enzyme opharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or Claim 1; SEQ ID NO 2461; 134pp; English more proteins.

Sequence 954 BP; 288 A; 198 C; 229 G; 239 T; 0 U; 0 Other;

S S 밁 밁 8 밁 á Query Match Best Local : Matches Local Similarity 121 181 61 94 34 954; ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTG CTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTTGTGG AGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCAC AGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAACCTACGGCGAAGAC AGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCAC ATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTG ilarity 100.0%; Conservative 77.6%; Score 954; DB 12; 100.0%; Pred. No. 2e-233; <u>.</u> Mismatches Length 954; Indels CGAAACCTACGGCGAAGAC <u>,</u> Gaps 153 60 93 240 273 180 213 120

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RESULT 6
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                                                                                                                                                                                                                                                                    Arabidopsis thaliana; thale cress; plant; transgenic; stress; metabolic pathway; biosynthetic pathway; nutr: insecticide; antibiotic; ds.
                         27-JAN-2000;
                                                                          26-JAN-2001; 2001US-00770149
                                                                                                                                                                                                                        Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana polynucleotide SEQ ID NO
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Matches 635
                                                                                                                                                                                                   The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABQ65427-ABQ66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                             Rameaka
Garcia C
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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HAMILTON C PRICE J L.
RAINES T M.
YU Y.
RAMEAKA J G.
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                                  ACTAAAAGTAGAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCT
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Page A, M
Kricker M,
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M, Slater T,
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Ledford BL, Woessne
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The invention relates to a recombinant polynucleotide comprising any or the 58798 Cotton plant cDNA sequences mentioned in the specification. Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having improved property. Producing a plant thaving an improved property comprises transforming a plant with a recombinant construct comprising promoter region functional in a plant cell operably joined to a
                                                                                                                                                                   New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway drought tolerance; plant disease resistance; galactomannan; lighir plant growth regulator; heat tolerance, herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed
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(ZHOU/)
(CAOY/)
                                                                                                                                       Claim
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CAO Y.
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                                                                                                           AGCTGGTCCATGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCT
                                                                                                                                                                                      TTACCTCATACAGGTACGAAGGAGATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTA
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The invention describes an isolated polynucleotide (I) comprising a nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse sequences, or sequences having 75, 90 or 95 % sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of
                                                                                                                                                                                                                                                                                                                                                                                                                                   programmed cell death; plant development; plant cell cycle; ATL2; Dnase; lls; lsdl; nucellin-like aspartic protease; annexin; prohib fen-like protein; rac2; retinoblastoma-related protein; SINA; TFII TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like prot gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulating seven in absentinia; transcription initiation factor;
                                                                                                                          altering the devel plant development.
                                                                                                  Claim
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                                                                                                                                       isolated polynucleotide useful for modulating programmed cell death, ering the development cycle of plant cells, and subsequently modifying
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Best Loc
Matches
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                                                                     ACTGGAACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTTGAGTTGACTTG
                                                                                                                   CAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAA
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                                                    CTGGGAACAGATGAATGGGCTCTTACCAGAGTAGTCACCACTCGTGCGGAAGTTGACATG
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Matches 666
                                                                                                                                                                                                                                                                                                      The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the
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The invention describes a nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to any one of 999 fully defined Arabidopsis thaliana sequences (I) as given in specification e.g., 360, CC 1137, 455, 219, 472 nucleotides, etc, or its fragment. (I) is useful as a lybridisation probe to complementary molecules in a cDNA library. (I) is also useful for generating genetically modified and transgenic organisms, comparison or modifier and plants. A proten encoded by (I) is useful in screening assays to determine the effect of candidate inhibitors, activators or modifiers of the gene product. The protein is also useful for screening assays to determine the effect of candidate inhibitors, activators or modifiers of the gene product. The protein is also useful for screening biologically active agents e.g., fungicides and concein acid, where the nucleic acid comprises transcription regulatory sequences operably linked to a sequence capable of hybridising under stringent conditions to (1) is useful in the study of genetic function and regulation, for alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene product. This sequence represents an Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorlach u,
Rameaka JG,
Parcia CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Arabidopsis thaliana nucleic acids useful genetically modified transgenic organisms, for a active agents such as fungicides, insecticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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(KRIC/)
(SLAT/)
(DAVI/)
(ALLE/)
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(WOES/)
(HAAS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
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(PAGE/)
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LEDFORD B L.
LEDFORD B L.
WORSSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HOFFMAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMILTON C M. PRICE J L.
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RAINES T M.
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487 BP;
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, Page A, Ma
Kricker M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function; genetic regulation; cellular metabolism;
  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44pp; English.
C; 88 G;
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Ledford BL, Woessner
, Davis KR, Allen K,
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JP, Haa
Hoffman
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Haas
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761 470;

CAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACTGATGAAG

Query Match Best Local S Matches 470

Similarity

38.2%; So larity 100.0%; I Conservative 0;

Score 470; DB 10; | Pred. No. 7.8e-110; 0; Mismatches 0;

Sequence

136

2

167 T; 0

U; 0 Other;

Length 487; Indels

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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing a
                                                       New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
                                                                                                                                                                                                                                                                                                    Eucalyptus
plant cell
                                        Claim
                                                                                                   P-PSDB;
                                                                                                                              Bloksberg LN;
                                                                                                                                                                              13-OCT-1998;
11-AUG-1999;
                                                                                                                                                                                                                               20-APR-2000
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                                                                                                                                                  (GENE-)
                                                                                                                                                                                                            08-OCT-1999;
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                                                                                                                                                                                                                                                                      Pinus radiata.
                                                                                                                                                                                                                                                                                       transgenic plant;
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                                       1; Page 93;
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                                                                                                                                                 GENESIS R
                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 1293
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99US-0148426P
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                                       301pp; English
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                                                                                                                                                                                                                                                                                                                                                   entry)
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Query Match
Best Local S
Matches 664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1293
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                                                                                                                                                               CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGG
                                                                                                                                                                                                                                                              TCTTGAGGAAGGAGATGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTG
                                                                                                                                                                                                                                                                                                                       ACAGGTCAATGCTACGCTGAATCACTACAAAAATGAGTTTGGAAATGATATCAACAAGGA
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CATTGGAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGA
                                                                                       AACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGT
                                                                                                                                       CCTGACTCGCCCTGAGAAGTATTTTGAAAAGGTTCTTCGTCTAGCCATCAATAAGCGAGG
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Pred. No. 2.5e
0; Mismatches
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                                                                                                                                                                                                       The present invention relates to coding sequences (see AAF44740-F44840 and AR744843-F44844) and proteins (see AAF5714-F65814) involved in programmed cell death (PCD; apoptosis). The coding sequences and proteins of the present invention are useful for modulating a PCD or cell death pathway and various developmental pathways in a forestry plant, by stably incorporating one of the present coding sequences into the genome of the forestry plant, where the coding sequence provides a PCD pathway that is not present in a native form of the forestry plant
                                                                                                                                                                                                                                                                                                                                                    Novel defender against cell death programmed cell death pathway and forestry plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF44756
                                                                                                                                                                                 Sequence 1293 BP; 359 A; 290 C; 313 G;
                                                                                                                                                                                                                                                                                                                            Claim 1; Page 54-55; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUN-2000; 2000WO-NZ000086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell death modulator; programmed cell death; PCD; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forestry plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Annexin-like protein coding sequence
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                                                                                                    30 AAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTTCTTGATGATGCTGAGCA
                                                                                                                                             Similarity
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                           GCTCCGGACAGCCTTCGCAGGATGGGGAACAAATGAGAAGCTGATCATATCCATATTGGG
                                                   ATTGAGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTGGC
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                                                                                                                                          38.1%;
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                                                                                                                                             Score 468.6; DB 4;
Pred. No. 2.5e-109;
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                   polynucleotide useful for modulating specific development pathways in
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XX ADB96
XX ADB96
XX DT 04-DE
XX DrogI
XX DrogI
XX DrogI
KW Dnase
KW fen-1
programmed cell death; plant development; plant cell cycle; ATL2; DAD1; Dnase; lls; lsd1; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma-related protein; SINA; TFIID;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated polymucleotide (I) comprising a nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse sequences, or sequences having 75, 90 or 95 % sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of the present invention to do with (I) sequences of plant cells, and altering plant development. This sequence encodes a protein associated with the programmed cell death pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide useful for modulating programmed cell altering the development cycle of plant cells, and subsequently more plant development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulat seven in absentinia; transcription initiation factor; testis enhanced gene transcript; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1293 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 28-29;
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                  TATGGCAAGACAAGCATATCATGCCCGATACAAGAAGTCAATGGAAGAGGACGTCGCTCA
                                        TCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCA
                                                                                                           GACTTCAAGCAACCAAGTTCTTATGGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCT
                                                                                                                                                         TTGGTCACTTGATCCGGCTGAACGTGATGCGTACTTGGCGAATGAAGCGACGAAAAGATG
                                                                                                                                                                                GTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTACAAAAAAGATG
                                                                                                                                                                                                                              GGACCTCCTCAAGGCATTGGACAGAGAACTTACCAATGATTTCGAGAGGCTGGTGGTCCT
                                                                                                                                                                                                                                                             AGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCTTGTT
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Pred. No. 2.5e-109;
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Matches 645; Conservative
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                CTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAACTGG
                                                                       GTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTACAAAAAGATG
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nilarity 67.2%;
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99US-0161993P.
99US-0162142P.
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Pred. No. 5.1e-106;
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Search completed: August 22, 2005, 07:26:19 Job time: 813 secs

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Result
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

## TINITION Arabidopais thaiiana Full-length cDNA Complete sequence from clone GSLTSII62ZB06 of Silique of strain col-0 of Arabidopais thaliana (thale cress) RESION BX818120.1 GI:42471185 SION BX818120.1 GI:42471185 SION BX818120.1 GI:42471185 ROBES Arabidopais thaliana (thale cress) Arabidopais thaliana (thale cress) Arabidopais thaliana (thale cress) REBENCE I (SEIT\_CNDA. REBENCE I (SEIT\_CNDA. REBENCE I (SEIT\_CNDA. ITHE Arabidopais thaliana (thale cress) REBENCE I (SEIT\_CNDA. I (Bases I to 1155) ITHE A (Seit\_CNDA. A (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., ITHE A (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., ITHE A (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Clepet,C., Schachter,V., ITHE A (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Scarpelli,C., Schachter,V., ITHE A (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C., Schachter V., Weissenbach J., Salanoubat,M., IVIE (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C., Schachter V., Weissenbach J., Salanoubat M., IVIE (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C., Schachter V., Weissenbach J., Salanoubat M., IVIE (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C., Schachter V., Weissenbach J., Salanoubat M., IVIE (Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C., Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C., Seit\_CNDA.) (Auny,J.M., Jaillon,O., Wincker,P., Seit\_M., Jaillon,O., Wincker,P., Seit\_M

/mol\_type="mRNA" /strain="Col-0"

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/tissue_type="Silique"
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- Web: www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 1095)

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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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TGTTATCTCTTATCTCCCCTCTCTCT-CTTTGATGAGTTTCAAATCGTTTGATTTTGTT
                                                                   GAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAAGATGCTCGTCGCACTTCTCGG
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                                                                                                                  TGAGATTGACTTGAAGGTCATTGGAGAGGAGGAGCACCAGCAGGAACAGCATTCCTTTGGA
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Pred. No. 1.4e-271;
0; Mismatches 1;
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Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.

URGY INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-NOV-2003) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1137)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTC; GSLT_cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Location/Qualifiers
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Direct Submission
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AAACACTAAAAGTAGAAGAAAAAATGG---CGACTCTTAAGGTT---TCTGATTCTGTTCCTG
                                                               AAACACTAAAAGTAGAAGAAAATAGAAAGACTCTTAAGGATAAAAAAATCTGTTCCTG
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                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                /clone="GSLTPGH18ZF02"
/tissue_type="Hormone '
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                            . .113/
/gene="At1g35720"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                       strain="Col-0"
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Pred. No. 1.9e-265;
0; Mismatches 20;
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                                                                    GTTTCTACA - AAAACCTTGTTTGTTTTTGTGTGTTTTTGAGTTCCTAA
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Annotation

Unpublished (2004)

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out

full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

Tenome released by MIPS (Munich Information center for Protein
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1063)
1 (bases 1 to 1063)
1 (Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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BX838972.1 GI:42533055
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Sequences).
http://www.genoscope.cns.fr/cyi-bin/ggb/ggb?source=Arabidopsis.
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CCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCACACTACCGGTGACTT
                                 CCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCACACTACCGGTGACTT
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/mol_type="mRNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
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        Unpublished 2 (bases 1
                                                                                                                                              BX815939.1 GI:42472187
                                                                                                                                                               966 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH18ZH06 of Hormone Treated Callus of Strain col-0 of Arabidopsis thaliana (thale cress).
                            Annotation
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libralities construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
GTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGC
                                                                                        GGAAATTCTCAAGAGTCTTGAGGAAGGAGGATGATGACAAGTTCCTTTGCACTTTTGAG
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                                                              GGAAATTCCCAAGAGTCTTGAGGAAGGAGATGATGACGACAAGTTCCTTGCACTTTTGAG
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/tissue_type="Hormone T
/plasmid="pCMVSPORT_6"
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/gene="At1g35720"
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                                                             The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboch W.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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1 (bases 1 to 1034)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

N Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                Submitted (18-NOV-2003) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNSO9Y3M 1034 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS23ZB01 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
                                http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
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BX841810.1 GI:42454468
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Arabidopsis thaliana
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/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clome="GSLTLS23ZB01"
/tissue_type="Adult vegetative tissue"
/plasmid="pCMVSPORT_6"
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Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 910 Std Error: 0
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 910)
Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-scale identification and analysis of genome-wide
single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF652924 910 bp mRNA linear EST 06-NOV-:
85-L020135w-066-001-IZ1-SP6P MPIZ-ADIS-066 Arabidopsis thaliana
CDNA Clone MPIZp2001IZ11Q 5-PRIME, mRNA sequence.
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                                                                                            /clone lib="MPIZ-ADIS-066"
/note="Vector: pcMvSpORT6; Site 1: Sal1; Site 2: Not1;
/note="Vector: pcMvSpORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from Arabidopsis thaliana, accession
Wassilewskija-0; roots from three weeks old plants grown
on MS-plates at 26M-0C with 16 hours light/day; library
was made at the Max-Planck-Institute for Plant Breeding
Research, Cologne, Germany; cloning sites Sal1-Not1,
primer sites and orientation:
SP6-Sal1-CCACGCGTCGG-Sprime-cDNA-polyA-CC-Not1-T7; GATEWAY
compatible; Note: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of high-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection' P1: Bernd Weisshaar Sequence submission managed
by RZPD/GABI-Primary database: http://gabi.rzpd.de
for further information."
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/lab_host="E. coli TOP10"
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/ecotype="Ws-0"
/db_xref="GABI:939529"
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/clone="MPIZp20011211Q"
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                    CNSOAC11 865 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSL/FEB69ZE06 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URCV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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HTC; GSLT cDNA.
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 (bases 1 to 865)
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/tissue_type="Flowers
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="At1g35720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Col-0"
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0; Mismatches 18;
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 843)
Schmid, K.J., Socrensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
                                                                                                                                                     12799357
Contact: Weisshaar B
COntsol DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                        Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabido Genome Res. 13 (6), 1250-1257 (2003)
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                                                                                             Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 843 Std Error: 0
Plate: 4 row: L column: 08
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CF652048.1
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                                                                             primer: SP6P;.
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/mol_type="mRNA"
                     organism="Arabidopsis thaliana"
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                                      AAGCAAAGCTCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAAT 680
                                                                                                                                                                                    TGAGAAAATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAG
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/db_xref="GABI:938637"
/db_xref="CABI:938637"
/db_xref="CABI:938637"
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/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: Not1;
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/clone_"Vector: pCMVSPORT6; Site_1: SalI; SalI; SalI; Site_2: Not1;
/clone_"Vector: pCMVSPORT6; Site_1: SalI; SalI
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Pred. No. 2.7e-206;
D; Mismatches 7;
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1 (bases 1 to 814)

Lundegaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S. and Welinder, K.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Aalborg Universitet
Sohngaardsholmsvej 49, 9000
Tel: +45 96358467
Fax: +45 98141808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Karen G. Welinder Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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011E11AF Infected Arabidopsis
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GCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCAAGCAAACCTACGGC
                                                       CAATTGAGAACCGCTTTTGAAGGATGGGGTACGAACGAGGACTTGATCATATCAATCTTG
                                                                                                AGGAAAATGGCGACTCTT-AGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAG
                                                                                                               AGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGTTCCTGCTCCTTCTGATGATGCTGAG
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                                                                                                                                                                                                                                                                                                                 /organism="Arabidopsis tl
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/dev_stage="Plant 3 weeks
                                                                                                                                                                                                                               /dev_stage="plant 3 weeks old, three days post infection" /clone_lib="Infected Arabidopsis Leaf" /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."
                                                                                                                                                                                                                                                                                                                                                                                               1. .814
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Pred. No. 2.3e-194;
0; Mismatches 3;
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RESULT 11
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AUTHORS
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            Aalborg Universitet
Sohngaardsholmsvej 4:
Sel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dl
                                                                                                                                                          Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 782)

Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S. and Welinder, K.G.
                                                                                                                                                                                                                                                                                                                   BU639010 782 bp mRNA linear EST 23-5
003A04 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA,
sequence.
BU639010
                                                                                      plants
Unpublished (2002)
Contact: Karen G. Welinder
Institut for bioteknologi
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              kgw@bio.auc.dk
Location/Qualifiers
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/mol_type="mcNA"
/mol_type="mcNA"
/cootype="Columbia"
/db xref="taxon:3702"
/db xref="taxon:3702"
/clone_lib="Infected Arabidopsis Leaf"
/clone_lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoracearum infected lea
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
selected."
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Pred. No. 3.1e-183;
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Sohngaardsholmsvej 49, 9000
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Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 775)
Lundsgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somervil and Welinder, K.G.
EST sequencing of Erysiphe cichoracearum infected Arabidopsis
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CGTTGCTCACCACACTACCGGTGACTTCAGAAAGCTTTTTGGTTTCTCTTGTTACCTCATA
                                                                                                                        TATCTTGTTGTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTAC
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                                                                                                                                                                                                                                                                                                       AATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAAC
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                                                            GCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGA
                                                                                                                                                                                                                                                                                      AATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAAC
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                                                                                                                                                                                                                              59.7%;
ilarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="Plant 3 weeks old, three days post infection" /clone_lib="Infected Arabidopsis Leaf" /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT
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/db_xref="taxon:3702"
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Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
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Pred. No. 8e-181;
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Spermatophyta, Magnoliophyta, eudicotyledons, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                           Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Functional Genomics Research
RIKEN Genomic Sciences Center
3-1-1 Koyaddai, Tsukuba, Ibaraki 305
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large scale analysis of Arabidopsis full-length Unpublished (2002) Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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AV784024 RAFL5 Arabidopsis thaliana
mRNA sequence.
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57.2%; Silarity 100.0%; Conservative 0;
                                                                                                /clone_lib="RAFL5"
/note="Site_1: SstI; Site_2: XhoI; subjected
dehydration-treated(1,2,5,10,24 hr)"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                               /dev_stage="rosette plants"
/lab_host="SOLR"
                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                       clone="RAFL05-15-G22"
                                                                                                                                                                                                                                                                 /organism="Arabidopsis
  Score 703; DB 1; Lo
Pred. No. 1.3e-172;
0; Mismatches 0;
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                                       Length 703
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507 CGAAGGAGATGAAGTGAACATGACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAA

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ACCESSION
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AV785121 RAFL6 F

mRNA sequence.

AV785121

AV785121.1 GI:1

EST.
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Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
                                                                              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y. Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                        Large scale analysis of Arabidopsis full-length Unpublished (2002)
                                                                                                                                                                       Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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 42
 TGTGGTCTCTTAAGTTATATATATATGAAGAGCATTGGCC
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Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACTGATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGG
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TGTGGTCTCTTAAGTTATATATATATATGAAGAGCATTGGCC
                                                       CTCTCTCTCTTTGATGAGTTTCAAATCGTTTGATTTTGTTTCTACAAAAACCTTGTTT
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/note="Site 1: SstI; Site 2:
dehydration 1, 2, 5, 10, 24
hr) treatments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="plants at various germination to mature seeds" /lab_host="DH10B"
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Pred. No. 7.8e-172;
0; Mismatches 0;
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
UNGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 679)
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BX836971.1 GI:42531054
EST.
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BX836971 Arabidopsis thaliana Clone GSLTLS38ZF07 SPRIM, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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GTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAAC 806
                                                                                                                                                                                                                                                                                                  AATCAAGGACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAA 626
                                                                           GAGTCTTGAGGAGAGGAGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCA
                                                                                                                                                                                                                      AGCTCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAA 686
                                                                                                                         GAGTCTTGAGGAAGGAGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCA 746
                                                                                                                                                                   AGCTCAGATCAATGCTACTTTTGACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAA 180
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/clone="GSLTIS38ZF07"
/tissue type="Adult vegetative tissue"
/clone Tib="Arabidopsis thaliana Adult vegetative tissue
col-0"
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/mol_type="mRNA"
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Pred. No. 2.1e-163;
0; Mismatches 7;
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Search completed: August 22, Job time : 4657 secs 2005, 10:19:14

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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           222222211111111
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                                                                                                468.6
208.4.2
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2: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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US-09-949-016-4306
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Sequence 17, Appl
Sequence 20, Appl
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Sequence 1149, Appl
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Sequence 1152, Appl
Sequence 1152, Appl
Sequence 101, Appl
Sequence 2431, Ap
Sequence 33, Appl
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GCAAGCT	CAACCAA	TGAACCC        TGATCCG	CAAGACT	TGCTGAA     TGCGGCG	AGCCTTC	GACTCTT        GACTCTC	38.1 68.4 vative	harry Annette Compos death 199 1199 1206 Or Wind		1301 1516 1957 1932 1300 5300 5300 2054 2120 2120 2120 21386 2386 2386 2386 2386 2386 2386 2386 2
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ATGCT	TATG	AGCGTV	;ACAAG     ;ACAGA	GGAAA       GGAAG	GATGG	FITTCIV	Score 468.6; Pred. No. 1.3e 0; Mismatches	932A 8 af heir 9/32	ALI	US-09-023-655-1190 US-09-919-172-38 US-09-949-016-4660 US-09-949-016-1750 US-09-949-016-1199 US-09-949-016-1199 US-09-949-016-1199 US-09-949-016-1199 US-09-949-016-1199 US-09-949-016-1199 US-09-949-016-1198 US-09-949-016-1198 US-09-949-016-4605 US-09-949-016-4605 US-09-910-147B-15 US-09-799-451-268 US-09-799-451-268 US-09-799-451-268
CGCTAC	JAAGTT     JAAATA	GATGCT	SAGCTO	GTCATO	GGTACC	GATTCI	468.6 No. 1 smatch	fecting use in 5,932A	ALIGNMENTS	99499999999999999999999999999999999999
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GENERAL INFORMATION:
APPLICANT: Lasham, Annette
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting pro
TITLE OF INVENTION: death and their use in the
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 789
TYPE: DNA
ORGANISM: Pinus radiata
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                                                                                                                   APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 704
TYPE: DNA
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-25-932A-21
; Sequence 21, Application
; Patent No. 6451604
; Patent NFORMATION:
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                                             Score 208.4; DB 3;
Pred. No. 5.1e-51;
0; Mismatches 226;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Plinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant (
FILE REFERENCE: 1022
CUCRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 484
LENGTH: 484
CORGANISM: Pinus radiata
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 233; Conserv
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Pred. No. 1.4e-44;
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Patent No. 6812339
GRMERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Matches
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SEQ ID NO 2091
LENGTH: 1332
TYPE: DNA
ORGANISM: Human
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
  474
                                         446
                                                                                                                                                              354 GGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGC
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                                         AGTATACAAGAAGAGTCTTGGAGATGACATTAGTTCCGAAACATCTGGTGACTTCCGGAA
                                                                                TCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCACACTACCGGTGACTTCAGAAA
                                                                                                                           TGAAATCTTAACTACCAGGACAAGCAGGCAAATGAAGGATATCTCTCAAGCCTATTATAC
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Pred. No. 2.1e-33;
0; Mismatches 468;
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RESULT 6
US-09-023-655-1149
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OCCUMENTATION SYSTEM: PC-DOS/MS-DOS
               ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
 TELEPHONE:
                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PALO ALTO
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US-09-023-655-1149
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Best Local Similarity 49.0%;
Matches 456; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1339 base pair
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IMMEDIATE SOURCE:
LIBRARY: GENBA
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                                                                        TAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCG
                                                                                                                                                   CTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACTGATGAAGGAGCACTCAC
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 CAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAGATTACGAGAA
                                       CCGAATAATGGTGTCCAGATCAGAAATTGACCTTTTTGGACATTCGAACAGAGTTCAAGAA
                                                                                                                TTTAGCCGAAAGACTGCATCGAGCCTTGAAGGGTATTGGAACTGATGAGTTTACTCTGAA
                                                                                                                                                                                           TGGGCATTTTGAAGACTTACTGTTGGCCATAGTTAATTGTGTGAGGAACACGCCGGCCTT
                                                                                                                                                                                                                              TGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAGGACA---AGCACTACAATGA
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Pred. No. 2.1e-33;
0; Mismatches 468;
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-10-33
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-722
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US-09-949-016-722
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 722
LENGTH: 1339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTACGAACGAGGACTTGATCATATCAATCTTGGCTCACAGAAGTGCTGAACAGAGGAA 173
                                                             GGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAGGACA---AGCACTACAATGA
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                      GGCCAAACAAGATGCCCAGATTCTCTATAAAGCTGGTGAGAACAGATGGGGCACGGATGA
                                                                                                    AGCTCTGTTGACTTTGGCAGATGGCAGAAGAGATGAAAGTCTGAAAGTGGATGAGCATCT
                                                                                                                                    GCTTTTGGTTTCTCTTGTTACCTCATACAGGTACGAAGGAGAGAAGTGAACATGACATT
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Pred. No. 2.1e-33;
0; Mismatches 468;
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US-09-023-655-1152
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US-09-325-932A-19
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SEQ ID NO 19
LENGTH: 221
TYPE: DNA
ORGANISM: Pinus 1
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Composi
TITLE OF INVENTION: death (
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Patent No. 6451604
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 169;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               831 TAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGGAGTACCAGCG
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1152, Application US/09023655
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                                                                                                    TGGTACCTCTTGTGAGCTCCTACCGTTATGATGGAGATGA
                                                                                                                            TGGTTTCTCTTGTTACCTCATACAGGTACGAAGGAGATGA 518
                                                                                                                                                                             ACAAGAAGTCGCTGGAAGACGTCGGTCACCACACACTGGAGATTTTCGTAAGTTGC 180
                                                                                                                                                                                                                  ACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCACACTACCGGTGACTTCAGAAAGCTTT
                                                                                                                                                                                                                                                           TAGCCTGCACGAGGTCTCCGCAGCAGTTGCTTATGGCAAGACAAGCATATCATGCCCGAT
                                                                                                                                                                                                                                                                                                                                       CGTACTTGGCGAATGAAGCGACGAAAAGATGGACTTCAAGCAACCAGGTTCTAATGGAAA
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Pred. No. 1.1e-30;
0; Mismatches 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 'Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9187137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PATELECOMMUNICATION INFORMATION: TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
Type: nucleic acid
single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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   AGATCATCTGCTCCAGAACCAACCAGGAGCTGCAGGAAATTAACAGAGTCTACAAGGAAA
                             AAGTTGCTTGCACAAGGACATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTC
                                                           ACGCTTCTGAGCTAAAAGCTTCCATGAAGGGGCTGGGGAACCGACGACGACTCTCTCATTG
                                                                                         ATGCTTTATTGGCTAATGAAGCTACAAAAAGGTTCGACTTCAAGCAACCAAGTTCTTATGG
                                                                                                                       CCTTATCTGGCCACCTGGAGACGGTGATTTTGGGCCCTATTGAAGACACCTGCTCAGTATG
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Pred. No. 5.3e-20)
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US-09-814-915A-101
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                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 101
LENGTH: 1362
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 101, Application US/09814915A Patent No. 6750015
GENERAL INFORMATION:
                                                                                          Matches
                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Horwitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone
TITLE OF INVENTION: Thereto
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2848-39
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GTACGAACGAGGACTTGATCATATCAATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAG 175
                                                                                          Conservative
                                                                                                       8.4%;
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CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 60/214,870
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
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                                                    ATTCTGTTCCTGCTCCTTCTGATGATGCTGAGCAATTGAGAACCGCTTTTGAAGGATGGG
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  ATACTAACTTTGATGCTGAGCGGGATGCTTTGAACATTGAAACAGCCATCAAGACCAAAG
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                                                                                                                                        Score 103.8; DB 4; Pred. No. 5.3e-20;
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                                                                                                                 Mismatches
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Sequence 2431, Application US/09949016
PATENT NO. 6812339
GENERAL IMFORMATION: Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
TITLE OF INVENTION: WITH HUMAN DISEASE, ME
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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US-09-949-016-2431
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PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 2431
LENGTH: 1614
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                                   TCAGAATCATGGTCTCCCGCAGTGAAGTGGACATGTTGAAAATTAGGTCTGAATTCAAGA 1041
                                                          CTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGGAGGAGGTACCAGC
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Pred. No. 5.9e-20;
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GENERAL INFORMATION: GENERAL REPLICANT: KASET, MATTHEW R.

FITTLE OF INVENTION: GENERS EXPRESSED IN TREAT

FILE REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401
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SEQ ID NO 393
LENGTH: 1660
TYPE: DNA
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Best Local :
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                        CTGATTGACCAAGATGCTCGGGATCTCTATGACGCTGGAGTGAAGAGGAAAGGAACTGAT
                                                                                           TTGGCTAAGCAAGAAGCTAAGCTGGTCCATGA---GAAAATCAAGGACAAGCACTACAAT
                                                                                                                               TGATGGTTGGCCCTGGCAAAGGGTAGAAGAGCAGAGGATGGCTCTGTCATTGATTATGAA
                                                                                                                                                                 TTTTGGTTTCTCTTGTTACCTCATACAGG----TACGAAGGAGATGAAGTGAACATGACA
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Pred. No. 1.
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APPLICANT: Tait, Jonathan

APPLICANT: Tait, Jonathan

APPLICANT: Tait, Jonathan

INFORMATION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITE

FILE REFERENCE: UOFW-1-13841

CURRENT APPLICATION NUMBER: US/09/324,096A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 981

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

FEATURE:
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Best Local Similarity
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LOCATION: (1)..(981)
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                                                                                                                                                               CTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAG
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Pred. No. 1.9e-19;
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Sequence 3, Application US/09324096A
Patent NO. 6323313
GENERAL INFORMATION:
APPLICANT: Talt, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENI
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 981
TYPE: DNA
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Best Local S
Matches 418
                                                                                                                 NAME/KEY: CDS
LOCATION: (1)..(981)
-09-324-096A-3
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18; Conservative
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                                                 Score 101.6; DB 3;
Pred. No. 1.9e-19;
0; Mismatches 484;
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GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
                                                                                                Sequence 5, Application US/09324096A Patent No. 6323313
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CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 981
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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Local Similarity 46.0%;
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Pred. No. 1.9e-19;
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Db 913 TCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGA 972

QY 973 GAAGATGA 980

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Db 973 GAAGATGA 980
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Search completed: August 22, 2005, 03:09:22
Job time: 260 secs

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Database
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08 PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

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13: /cgn2_6/ptodata/2/pubpna/US09 PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B PUBCOMB.seq:*

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24: /cgn2_6/ptodata/2/pubpna/US1NAF PUBCOMB.seq:*

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26: /cgn2_6/ptodata/2/pubpna/US00 NEW_PUB.seq:*

26: /cgn2_6/ptodata/2/pubpna/US0 NEW_PUB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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473.4	479.6	479.6	479.6	497.8	635	1230	Score
38.5	39.0	39.0	39.0	40.5	51.6	100.0	Query Match
1058	1393	1145	1145	1184	635	1230	Query Match Length DB ID
14	18	18	18	19	ø	21	BB
4 US-10-219-220-218	US-10-424-599-1190	US-10-425-114-29928	US-10-425-114-7439	US-10-767-795-4242	US-09-770-149-655	21 US-10-690-564-1	Length DB ID
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45	44	43	42	41	40	39	38		36	35	34	33	32	31	30	29	28		26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10		<b>&amp;</b>
270.6	271	273.2	276.2	7	277.8	77.	82.	84.	84.	296.4	11.	15.	22.	24.	326	327	27.	336.2	w	338.6	338.6	•	•	•	346.6	346.6	w	ന	•	364.2	•	$\sim$	$\sim$	468.6	68.	7	471.8
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0-393-840-	-10-021-323-	-10-424-599-137	US-10-424-599-68473	-10-424-599-	0-424-599-137	-10-425-114-	-10-021-323-	-10-739-930-	0-425-114-798	-10-424-599-8858	-10-424-599-300	0-021-323-1552	0-021-323-1562	-10-437-963-7830	-10-021-323-1346	-10-021-323-	-10-021-323-1211	-10-437-963-5874	-10-739-930-227	-10-425-115-6369	-10-767-701-1454	-10-425-115-217	-10-767-701-1352	-10-425-114-2680	-10-425-114-2336	-10-425-114-219	-10-425-114-3528	-10-425-114-1022	-10-393-840-11	-10-393-840-	-10-219-220-2	-10-424-599-7045	-10-425-114-10	0-393-8	-10-219-220-	-09-770-96	
equence	quence 8405,	equence	e 68473	Sequence 130903,	Sequence 137007,	equence 13073,	equenc	equence 3735,	equence 7980, A	equence 8858	equence 30062,	e 15526,	equence 15621,	equence 78307,	e 13465,	equence 15046,	equence 12115,	equence 58743,	equence 2276, F	e 63693,	e 14545,	equence 2178, A	e 13525,	equence 26803,	e 23365,	e 21986	e 35285,	e 10228,	e 112, Ap	e 26	equence 20, App	equence 70457,	equence 10772,	equence 109, Ap	equence 17, App	quence 765, A	Sequence 28, Appl

## ALIGNMENTS

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US-10-690-564-1
                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/690,564
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Kopatentin 1.71
SEQ ID NO 1
LENGTH: 1230
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10690564
Publication No. US20050089872A1
GENERAL INFORMATION:
APPLICANT: KOREA KUMHO PETROCHEMICAL CO., LTD
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ANNEXINS FROM PLANTS
FILE REFERENCE:
FILE REFERENCE:
                                                                                                                                                        Query Match
Best Local Similarity
Matches 1230; Conserv
  61
                      61 GTTCCTGCTCCTTCTGATGATGCTGAGCAATTGAGAACCGCTTTTTGAAGAGATGGGGTACG 120
                                                                                                1 CCACGCGTCCGAAACACTAAAAGTAGAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCT
GTTCCTGCTCCTTCTGATGATGCTGAGCAATTGAGAACCGCTTTTGAAGGATGGGGTACG
                                                                   CCACGCGTCCGAAACACTAAAAGTAGAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCT
                                                                                                                                                      100.0%; Score 1230; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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                                           TGATTTTGTTTCTACAAAAACCTTGTTTGTTTTCTGTGTGTTTTGAGTTTCCTAAATAA
                                                                                                                                                              TCTACAGCTTCTGTTATCTCTCTCTCTCTCTCTCTTTGATGAGTTTCAAATCGTT
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CATTGGCCTAAAAAAAAAAAAAAAAAAAAAA 1230
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                                                                                     TGATTTTGTTTCTACAAAAACCTTGTTTGTTTCTGTTGTGTGTTTTGAGTTCCTAAATAA
                                                                                                                                                GCACTTCTCGGTGAAGATGATGCTTAATCAATCAATCCTCCACAGAGAAACATAAGCTGC
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APPLICANT: HOFFman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013RV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 655
LENGTH: 635
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-149-655
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Best Local Similarity
Matches 635; Conserv
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Kricker, Maja
Slader, Ted
Davis, Keith R.
Allen, Keith
TCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAA
                                                                 GAAACCTACGGCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAG
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                                                ATATCAATCTTGGCTCACAGAAGTGCTGAACAGAGGAAAGTCATCAGGCAAGCATACCAC
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Hamilton, Carol I
Price, Jennifer I
Raines, Tracy M.
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US-10-767-795-4242
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APPLICANT: KOVALIC,
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 4242
LENGTH: 1184
TYPE: DNA
ORGANISM: Gossypium hirsutum
FEATURE:
FORMATION OF THE COURT COUNTY CO
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Best Local Similarity 70.7
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                                                                                                                                   TCGAGAGAGCTATCTTGTTGTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTA
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70.7%;
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Pred. No. 2.3e-130;
0; Mismatches 282;
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; OTHER INFORMATION: Clone ID: US-10-425-114-7439
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US-10-425-114-7439
                                                                                Best Loca
Matches
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7439
LENGTH: 1145
TYPE: DNA
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Publication No. US20040034888A1
                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
                                                                                                                                                                                                          ORGANISM: Glycine max FEATURE:
                                                                                                      Local Similarity
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                     ACACTAAAAGTAGAAGAAAAATGGCGACTCTTAAGGTTTCTGATTCTGATTCCTGCTCCTT
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
AAACAAAAAACAGAACAATGGCGACACTTAAGGTTCCTCAGCCTCTTCCCCCCCGTTG
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                                                                                Score 479.6; DB 18
Pred. No. 3.3e-125;
0; Mismatches 299;
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RESULT 5
US-10-425-114-29928
US-10-425-114-29928, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong; APPLICANT: Zhou, Yihua
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; FEATURE:
; OTHER INFORMATION:
US-10-425-114-29928
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
FULE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 29928
LENGTH: 1145
TYDEE, NNA
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Best Local
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ORGANISM: Glycine
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US-10-424-599-1190
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 1190
LENGTH: 1393
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Best Local
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ORGANISM: Glycine
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                                              CATCAACGCAGCTGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTG 433
                                                                                                           AGAGAGCTATCTTGTTGTGGACTCTTGAACCCGGTGAGGGTGATGCTTTATTGGCTAATG
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                   CCTCTGAACAATTGTTTGCTGCGAGGAAGGCTTACCATGTTCTTTATAAGAAGTCTCTGG
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                                                                                                                                                                                                                                                      FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 218
SEQ ID NO 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 218, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                         Matches
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Best Local
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APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
                                                                                                                                                                                                      LENGTH: 1058
TYPE: DNA
ORGANISM: Eucalyptus
                                                                                                                                       Local Similarity
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Pred. No. 1.8e-123;
0; Mismatches 296;
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Sequence 28, Application US/10393840
Publication No. US20030229922A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Cell Wa
FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
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PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 09/170,862
PRIOR PILING DATE: 1998-10-13
PRIOR PILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR TILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR PILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 956
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 28
SEQ ID NO 28
LENGTH: 2588
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                        CCTGACTCGCCCTGAGAAGTATTTTGAAAAGGTTCTTCGTCTAGCCATCAATAAGCGAGG
                                                     СТТGАСААGAССАGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGG
                                                                                                        TCTTGAGGAAGGAGATGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTG
                                                                                                                                                        ACAGGTCAATGCTACGCTGAATCACTACAAAAATGAGTTTGGAAAATGATATCAACAAGGA
                                                                                                                                                                                      TCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAG
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APPLICANT: Huffman, Neil
APPLICANT: Huffman, Neil
APPLICANT: Hurban, Patrick
ITITE OF INVENTION: Expressed Sequences of Arabidopsis
ITITE OF INVENTION NUMBER: US/09/770,961
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 765
LENGTH: 487
TYPE: DNA
TYPE: DNA
TYPE: DNA
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US-09-770-961-765/c
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Best Local Similarity
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                                                                                                                                   GAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGG
   Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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                                                            AGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAG
                                                                                                           GAGCACTCACTAGAATTGTGACCACAAGAGCTGAGATTGACTTGAAGGTCATTGGAGAGG
                                                                                                                                                                                CAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACTGATGAAG
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                                       AGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACTCGTGGAG
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Kricker, Maja
Slader, Ted
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Rameaka, Joshua G.
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Publication No. US20030082724A1
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEO ID NOS: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 17
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Best Local Similarity 68.4%;
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TYPE: DNA
ORGANISM: Pinus radiata
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                                   TCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCA 449
                                                                       GACTTCAAGCAACCAGGTTCTCATGGAAATAGCCTGCACGAGGTCTCCGCAGCAGTTGCT
                                                                                            GACTTCAAGCAACCAAGTTCTTATGGAAGTTGCTTGCACAAGGACATCAACGCAGCTGCT
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GENERAL INFORMATION:

APPLICANT: Bloksberg, Leconard N.

ITILE OF INVENTION: Materials and Methods for the

FITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

FILE REFERENCE: 11000.1012c3

CURRENT APPLICATION NUMBER: US/10/393,840

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 09/636,800

PRIOR APPLICATION NUMBER: US 09/170,862

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR FILING DATE: 1999-01-00

PRIOR FILING DATE: 1999-01-00

NUMBER OF ESG ID NOS: 956

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH. 1093
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US-10-393-840-109

Sequence 109, App

Publication No. 1

GENERAL INFORMAT

APPLICANT: Blok

TITLE OF INVENT:

TITLE OF INVENT:

FILE REFERENCE:

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US-10-393-840-109
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Best Local Similarity
Matches 664; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NO 10772
LENGTH: 1145
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFO--
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              AGGAAATTCTCAAGAGTCTTGAGGAAGGAGGATGATGATGACAAGTTCCTTGCACTTTTTGA
                                                              CCACAAGAAGCAAAGCTCAGATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCG
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Pred. No. 6.6e-117;
0; Mismatches 311; ]
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RESULT 13
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APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT APPLICATION SEQ ID NOS: 285684

SEQ ID NO 70457

LENGTH: 1321

TYPE: DNA
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Best Local Similarity
Matches 644; Conserv
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386 TGCTTCACGCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTG
                                                                                                                                                                                                                                                                                206 GCGAAGACCTTCTCAAGACTCTTGACAAGGAGCTCTCTAACGATTTCGAGAGAGCTATCT
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                                                                           TGTTGTGGACTCTTGAACCCGGTGAGCGTGATGCTTTATTGGCTAATGAAGCTACAAAAA
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Pred. No. 2.7e-111;
0; Mismatches 312;
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; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Pinus radiata
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                                                           Query Match
Best Local Similarity
Matches 508; Conserv
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                                                                                                                                                                                                                                  APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT FILING DATE: 2002-08-14
ERIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR PILING DATE: 1999-06-04
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Pred. No. 1.7e-92;
0; Mismatches 218;
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                                            PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILLING DATE: 2000-08-10
PRIOR PELICATION NUMBER: US 09/170,862
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR FILLING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILLING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 956
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 26
LENGTH: 789
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/10393840 Publication No. US20030229922A1
                                                                                                                                                                                             APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides
FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
CURRENT FILING DATE: 2003-03-20
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Adj638872 Plant lip
Adn74567 Thale cre
Aag098199 Arabidops
Aag08873 Arabidops
Aab16294 Eucalyptu
Aab16294 Eucalyptu
Aab16321 pinus rad
Aab65730 Annexin-1
Adb94698 Programme
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XX AAGG
XX Prot
XX Pro
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05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

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17-APR-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO:
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transgenic plant.
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                                                                                      plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                           Arabidopsis thaliana
                                                                                                                                                   Thale cress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New lipid metabolism proteins and nucleic acids, useful in producitransgenic plants with increased levels of seed storage compound, lipid, a fatty acid, a starch or a seed storage protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 74; 115pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              he invention relates to novel isolated lipid metabolism proteins (IMP) nd encoding nucleic acids comprising a polynucleotide sequence encoding polypeptide that functions as a modulator of seed storage compounds in plant. The LMP nucleic acid is useful in producing transgenic plants ith increased levels of seed storage compound, e.g. lipid, a fatty acid, starch or a seed storage protein, as markers for specific regions of he genome and for evolutionary and protein structural studies. The resent sequence represents an LMP of the invention.
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                                                                                                                                                protein repressed
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                                                                                                                                             in E2Fa/Dpa expressing plants SeqID 2462
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Pred. No. 1.2e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generating transgenic plants for the production of growth regulators, certaing transgenic plants for the production of growth regulators, where certaing transgenic plants for the product and animal feed products, where characteristics are selected from increased yield or compass, enhanced survival capacity, stress tolerance, plant architecture corpsisiology, altered endoreduplication, biochemistry, signal curansduction, storage lipid mobilisation and/or altered photosynthesis, ceach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers curing transformation of cells or tissues. The identified genes play a crole in a variety of biological processes such as DNA replication, cell curanscription factors. This polypeptide sequence is thale cress protein expressed by a gene repressed 1.3 fold or more in plants overexpressing the E2Fa/DPa transcription factor, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Altering plant characteristics, useful for producing plants for enzyme opharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 317
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RGDYEKMLVALLGEDDA 317
                                                                            TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                                        DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEBILKSLEEGDDDDKFLALLRSTIQCL
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                                                  TRPELYFVDVLRSAINKTGTDEGALTRIVTTRABIDLKVIGBEYQRRNSIPLEKAITKDT
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standard; protein; 327 AA.  (c) (first entry)  is thaliana protein fragment SRQ ID NO: 7038.  (dentification; signal transduction pathway; metabolic pathway; tion assay; genetic mapping; gene expression control; promoter; lon sequence.  (c) 2008EP-00301439.  (c) 99US-012162548 (c) 99US-012162648 (c) 99US-012162648 (c) 99US-012162648 (c) 99US-012162649 (c) 99US-012162649 (c) 99US-01216649 (c) 99US-0121669 (c) 99US-0
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27-AUG-1999

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99US-0151333P
99US-01537519
99US-0154738P
99US-01537513P
99US-01557868P
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99US-01567586P
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99US-0158232P
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Pred. No. 1.3e-139;
Mismatches 0;
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33-JUN-1999
30-JUN-1999
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99US-0121825P
99US-0123180P
99US-0125788P
99US-0125785P
99US-0126264P
99US-0127462P
99US-0129845P
99US-0130047P
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99US-0130449P
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nilarity 100.
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-0149930P
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                          .0%;
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                Score 1611; DB 3;
Pred. No. 1.3e-139;
; Mismatches 0;
                                  Length
                  Indels
                                     328;
                 0;
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10-JUN-1999
11-JUN-1999
12-JUN-1999
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99US-01138540P 99US-0139147P 99US-0139452P 99US-0139454P 99US-0139454P 99US-0139454P 99US-0139454P 99US-0139462P 99US-0139462P 99US-0139462P 99US-0139462P 99US-0139462P 99US-0140353P 99US-0140823P 99US-0140823P 99US-0140823P 99US-0140823P 99US-014284P 99US-014284P 99US-014284P 99US-014331P 99US-014332P 99US-0144332P 99US-0144332P 99US-0144333P 99US-0144333P 99US-0144332P 99US-0144332P 99US-0144332P 99US-0144332P 99US-0144332P 99US-0144332P 99US-0145918P 99US-0145918P 99US-0146388P 99US-0146388P 99US-0147308P 99US-0147308P

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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polypeaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are
                                                                                                                                                                                     New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
                                                                                                                                                                                                                                                  WPI; 2000-339328/29
N-PSDB; AAA67100.
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plant cell
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11-AUG-1999;
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                                          AAB16321;
                                                           AAB16321 standard;
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SEQ ID NO:114
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Eucalyptus grandis; pinus radiata; Monterey pine; modification;
plant cell wall; polysaccharide; polysaccharide biosynthetic pa
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   transgenic
plant.
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pathway;

RESULT 8
AAB16321
ID AAB3
XX AAB1
AC AAB3
XX Ence
DY 31-C
DY 31-C
DY SINC
XX Ence
KW Plas
XX Ence
KW Plas
XX Fin
XX Ence
XX En 13-OCT-1998; 11-AUG-1999; Bloksberg (GENE-) 20-APR-2000 Pinus WO200022092-A2 radiata. GENESIS RES & DEV CORP LTD FLETCHER CHALLENGE FORESTS 98US-00170862. 99US-0148426P. 99WO-NZ000169 LTD.

New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.

WPI; 2000-339328/29. N-PSDB; AAA67128.

Claim 17;

Page

94-95; 301pp;

English

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA679070, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
  WPI; 2001-061724/07
                               Flinn
                                                                                                     04-JUN-1999;
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                                                                                                                                                                                                                                                            Cell death modulator; programmed cell death; PCD; apoptosis;
                                                                                                                                                                                                                                                                                         Annexin-like protein
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                                                          RES & DEV CORP LTD.
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Matches 226
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                                                                                                                                             programmed cell death; plant development; plant cell cycle; ATL2; DAD1; Dnase; lls; lsdl; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma related protein; SIMA; TFIID; TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like protein; gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1; defender against cell death; lethal leaf spot; lesion stimulating death; seven in absentinia; transcription initiation factor;
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Similarity 71.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARQAYHARYKKSMEEDVAHHTTGDFRKLLVPLGSSYRNDGDEVNMTLAKAEAKILHEKIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKAYGHEDLIRILATRSKAQVNATLNHYKNEFGNDINKDLKT-DPKDAFLTILRATVKCL
                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                              gene transcript.
                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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Pred. No. 3.8e.
99; Mismatches
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US2003082724-A1

Pinus

radiata.

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RESULT 11
ADB94896
ID ADB94
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AC ADB94
XX
O1-DE94
XX
DT 04-DE
DX
DE Progr
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KW Drogr
KW Drase
KW TEGT,
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KW Gp 91
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated polynucleotide (I) comprising a nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse sequences, or sequences having 75, 90 or 95 $ sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of the present invention to do with (I) are useful for modulating programmed cell death and thereby altering the development cycle of plant cells, and altering plant development. This is the amino acid sequence of a protein associated with the programmed cell death pathway.
programmed cell death; plant development; plant cell cycle; ATL2; DAD1; DASS; l18; l8d1; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma-related protein; SINA; TFIID; TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like protein; gp 91 NADPH oxidase subunit; NPR-like protein; BAG-1;
                                                                                                                          04-DEC-2003
                                                                                                                                                                                   ADB94896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 47-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated altering the
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                                                                                                                                                                                                                                                                                                                                                                                               DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                       RGDYEKMLVALLGEDDA
                                                                                                                                                                                                                                                                                                                                 TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
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                                                                                                                                                                                                                                                                                                                    TRPEKYFEKVLRLAINKRGTDEGALTRVVATRAEVDMKFISEEYQRRNSIPLDRAIVKDT
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                                                                                         cell death pathway protein annexin
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                                                                                                                                                                                  protein;
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71.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1171.5; DB; Pred. No. 3.8e-99; 39; Mismatches 51
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RESULT 12 AAG09201 ID AAG09 XX

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Best Local Similarity
Matches 218; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide useful for modulating programmed cell death, altering the development cycle of plant cells, and subsequently modifying plant development.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Fig 27; 214pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          defender against cell death; lethal leaf spot; lesion stimulating death; seven in absentinia; transcription initiation factor; testis enhanced gene transcript.
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                     RGDYEKMLVALLGEDDA 317
                                                          MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
SGDYKKMLLALVGHEDA
                                                                                                                  EKAYNHDELIRIVTTRSKAQLNATLNYYNNEFGNAINKDL-KADPNDEFLKLLRSAIKCL
                                                                                                                                      DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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                                                                                                                                                                                                                                           LLKALDKELSSDFERSVLLWTLDPAERDAFLSNEATKRLTSSNWVLMEIACTRSSMELFM
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                                                                                                                                                                                                                                                                                                   MATIAVPPSVPSPAEDAEQLQKAFAGWGTNEDLIISILAHRNAAQRKVIRQTYAETYGED
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                                                                                                                                                                                                                                                                                                                                                            70.3%; Score 1132.5; 68.8%; Pred. No. 1.56 tive 48; Mismatches
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.5e-95;
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99US-0139462P.	99US-0139460P.	9908-0139459P.	99US-0139457P.	99US-0139456P.	99US-0139455P.	9905-0139492P. 9915-0139492P.	99US-0139453P.	99US-0139452P.	99US-0139119P.	99US-0138847P.	9905-01385400	99US-0137724P.	9903-0137502P.	99US-0137528P.	99US-0137222P.	99US-U136392P.	990S-0136021P.	99US-0135629P.	99US-0135353P.	9905-0134941F. 9905-0134941F.	9905-0134768P.	99US-0134370P.	99US-0134221P.	99US-0134219P.	99US-0134230F.	9905-01343550	99US-0132487P.	99US-0132486P.	99US-0132485P.	9905-0132484P.	9905-013248P.	99US-0131449P.	99US-0130891P.	9908-0130510P.	9905-01300//F:	9905-0129845P.	99US-0128714P.	99US-0128234P.	99US-0127462P.	9905-0126264P.	99US-0125788P.	9905-0123548P.	99US-0121825P.		2000ED-00301439				thaliana.	quelice.	netic mapping; gene expression	n; signal transduction pathway; metabolic	thaliana protein fragment SEQ ID NO: 7040.	(LIFBC entry)		
PR	PR:	אַק אַק	PR PR	PR	PR ?	B PR	PR	PR	PR :	PR	אָל פּ	g PR	PR	PR	PR	8 %	PR	PR	PR	ב ב	g p	PR	PR	PR.	אַ ק	3 5	2 PR	PR	PR	PR TR	8 8	景	PR	PR	, K	멅	PR	PR	קי קי	PR	PR	PR	g p	PR	אַ אַ	PR	PR	B 15	PR	<b>7</b>	PR	PR	PR	2 2	PR	PR
AUG-1	23-AUG-1999;	AUG-1	AUG-1	AUG-1	17-AUG-1999:	13-AUG-1999;	13-AUG-1999;	12-AUG-1999;	11-AUG-1999;	10-AUG-1999;	09-AUG-1999;	06-AUG-1999;	06-AUG-1999;	05-AUG-1999;	05-AUG-1999;	04-AUG-1999;	03-AUG-1999;	2-AUG-1	2-AUG-1	3-200-1	7-301-1	7-501-1	7-JUL-1	6-JUL-1	1 - JUL - 1	3 - JUL - 1	1 1 1 1 1	2-JUL-1	2-JUL-1	JUL-1	JUL-1999	JUL-1999	.999		20-JIII-1999;				19-,707-1399;	ديو ه	JUL-1	15-JUL-1999;	141	2-JUL-1	09-,717,-1999;	6-JUL-1999	2-JUL-1999	01-JUL-1999;	0-JUN-1	29-JUN-1999;	4-JUN-1999	23-JUN-1999;	Į.	18-JUN-1999;	- N	-JUN-1
0150566	99US-0149902P.	0149929	0149722	0149426	0149175	0148684	0148565	0148341	0148319	0148171	.0147493	0147416	-0147303	0147260	0147192	0147204	-0147038	0146389	0146388	7857760	-0145919	0145918	0145913	0145276	.0145210	0145145	-0145192	0145089	0145087	-0145085	0145086	-0144814	-0144884	-0144632	0144353	-0144334	-0144333	-0144332	-0144731	-0144086	-0144085	-0144005	-0143542	-0142977	-0142603	-0142390	-0142055	0141842	0141287	-0140823	-0140695	-0140354	-0139899	-0139817	-0139750	-0139463

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Query Match 66.5%; Sometime 100.0%; I Matches 211; Conservative 0;
                                                                                                                                                                                                   MEVACTRTSTQLLHARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMT
                                                                                                             RNSIPLEKAITKDTRGDYEKMLVALLGEDDA
                         RNSIPLEKAITKOTRGDYEKMLVALLGEDDA
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99US-0151066P

99US-0151060P

99US-0151438P

99US-0151438P

99US-0153070P

99US-0153070P

99US-0154039P

99US-0154779P

99US-0155486P

99US-0155486P

99US-01555659P

99US-0157117P

99US-01578659P

99US-0158029P

99US-0158029P

99US-0158029P

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99US-0159233P

99US-0159331P

99US-0159331P

99US-0160761P

99US-0160761P

99US-0160761P

99US-0161361P

99US-0161361P
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                           211
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  RESULT 13
AAGO 8875
ID AAGO 8875
AAGO 8875
AC AAGO 8
XX AAGO 8
AX AAGO 8
A
  25-FBB-1999
09-MAR-1999
09-MAR-1999
23-MAR-1999
23-MAR-1999
25-MAR-1999
16-APR-1999
11-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
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24-MAY-1999
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irplekaitkorrednykmivalicebbá 211  (first entry)  thaliana protein fragment SEQ ID NO: 3040.  tification; signal transduction pathway; metabolic pathway; sequence.  sequence.  2000EP-00301439.  99US-01121625.  99US-0123548P.  99US-0123548P.  99US-0123548P.  99US-012474P.  99US-012474P.  99US-012474P.  99US-012474P.  99US-012474P.  99US-012474P.  99US-012474P.  99US-012474P.  99US-012514P.  99U	RNSIPLEKAITKDTRGDYEKMLVALLGEDDA 317
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annexin XIIIa - do
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annexin III - huma
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annexin III - rat
annexin XI - human
annexin XI form B
annexin VI - mouse
annexin VII, long
annexin XI - xabbi
annexin XI - xabbi
annexin XI - mouse
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## ALIGNMENTS

probable annexin protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C;Accession: C86479

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: C86479

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A;Molecule type: DNA
A;Residues: 1-317 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9SYT0; GB:AE005172; NID:g8778967; PIDN:AAF79882.1; GSPDB:G
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                                                                           TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                              DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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100.0%; Pred. No. 1.6e-97;
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fiber annexin - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Acces: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31428
R;Shin, H.; Brown, R.M.
submitted to the EMBL Data Library, February 1997
A;Reference number: Z21028
A;Accession: T31428
A;Ccession: T31428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-316 <SHI>
A;Cross-references: UNIPROT:OB2090; EMBL:U89609; NID:g3493171; PID:g3493172
A;Experimental source: strain Texas Marker1
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding
                                    annexin upland cotton (fragment)
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999;
C;Accession: T10805
R;Potikha, T.S.; Delmer, D.P.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z17161
A;Accession: T10805
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T10805
A;Residues: 1-315 <POT>
A;Cross-references: UNIFROT: P93157; EMBL:U73746; NII
A;Experimental source: strain Acala SJ-2; cotton fil
C;Genetics:
A;Note: Annchl
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding
F;85-156/Domain: annexin repeat homology <AXR>
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                          Note: AnnGh1
Note: AnnGh1
Superfamily: annexin I; annexin repeat homology
Keywords: calcium binding
A5-156/Domain: annexin repeat homology <AXR>
 Query Match
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Score 1128.5; DB Pred. No. 3.4e-66;
                                                                                                                                                                      from GB/EMBL/DDBJ
                                                                                                              EMBL:U73746; NID:g1843524; PID:g1843525 SJ-2; cotton fiber
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C;Species: Capsicum a
C;Date: 15-Feb-1997 #
C;Accession: S66274
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A, Status: preliminary; nucleic acid sequence not shown
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-314 <PRO>
A, Cross-references: UNIPROT: 042657; EMBL: X33308; NID: 91071659; PIDN: CAA63710.1; PID: 9107
A; Note: the sequence of residues 155-230 is shown in line for annexin (alfalfa) rather t
C, Superfamily: annexin repeat homology
F; 14-85/Domain: annexin repeat homology <AX1>
F; 66-157/Domain: annexin repeat homology <AX3>
F; 169-238/Domain: annexin repeat homology <AX3>
F; 242-313/Domain: annexin repeat homology <AX4>
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A;Title: Characterization and gene expression of an annexin during fruit A;Reference number: S66274; MUID:96198603; PMID:8925897
A;Accession: S66274
                                                                                                                                                                                                                                                                                                    RPELYFVDVLRSAINKTGTDEGALTRI VTTRAEIDLKVI GEEYQRRNS I PLEKAITKDTR
                       TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                          DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
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VYPEHYFVEVLRDAINRRGTEEDHLTRVIATRAEVDLKIIADEYQKRDSIPLGRAIAKDT
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                                                                                               DKAYSDDEVIRILATRSKAQLNATLNHYKDEHGEDILKQLEDGDE---
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#sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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RGDYEKMLVALLGEDD

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annexin, isoform P35 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Bate: 20-Sep-1999 #sequence revision 20-Sep-1999 #text
C;Batcession: T06322; S11463; S11462
R;Lim, E.K.; Roberts, M.R.; Bowles, D.J.
J. Biol. Chem. 273, 34920-34925, 1998
A;Title: Biochemical characterization of tomato annexin
A;Reference number: Z15591; MUID:99074266; PMID:9857021
A;Accession: T06322
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A; Experimental source: strain Acala SJ-2; cotton fiber
C;Genetics:
A;Note: AnnGh2
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding
C;Keywords: calcium binding
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A;Cross-references: UNIPROT:081535; EMBL:AF079231;
A;Experimental source: tissue type root
R;Smallwood, M.; Keen, J.N.; Bowles, D.J.
Biochem. J. 270, 157-161, 1990
                                                                     A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-315 <LIM>
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A;Accession: T10807
A;Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLKVPVHVPSPSEDAEWOLRKAFEGWGTNEQLIIDILAHRNAAORNSIRKVYGEAYGEDL
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Pred. No. 8.3e-65;
3; Mismatches 53;
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n 16-Jul-1999 #text_change 09-Jul-2004
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                                                    NID: 93378203;
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                                                      PIDN: AAC97493.1;
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SNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHARQAYHARY 129 VPSPSEDSEQLRGAFQGWGTNEGLIISILAHRNAAQRKSIRETYTQTHGEDLLKDLDKEL

62

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annexin - alfalfa (fragment)
(;Species: Medicago sativa (alfalfa)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_char
C;Accession: T09552
R;Pirck, M.; Hirt, H.; Heberle-Bors, E.
Plant Physiol. 104, 1463-1464, 1994
A;Title: The cDNA sequence encoding an annexin from Medicago
A;Reference number: Z16735; MUID:94286751; PMID:8016273
                                                                                                                          C;Superfamily: annexin I; annexin repeat homology C;Keywords: calcium binding; phospholipid binding F;7-78/Domain: annexin repeat homology <AXR>
                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <PIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: annexin I; annexin repeat homology C;Keywords: calcium binding; phospholipid binding F;86-157/Domain: annexin repeat homology <AXR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Purification and partial sequence analysis of plant annexins.
A;Reference number: $11461; MUID:90372908; PMID:2396974
A;Accession: $11463
A;Mccession: $11461
A;Residues: 108,'X',110,'X',112-119,'X',121-127,'R',129,'X',131-133,'HI',136-141,'S',A;Accession: $11462
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A; Residues: 'EXNI', 175-177, 'EX', 180-181, 'X', 183-184, 'N', 186-192, 'L', 194-195, 'X', 197, 'X'
                                                        Matches
                                                                     Query Match
Best Local
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Best Local Similarity
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10 VPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGEDLLKTLDKEL
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                                                    Conservative
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Pred. No. 4.7e-63;
7; Mismatches 59;
                                                                     Score 1067.5; D
Pred. No. 3e-62;
                                                    Mismatches
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annexin-like protein - Arabidopsis thaliana
N;Alternate names: protein T31P16,220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50027
R;Bevan, M; Zimmermann, W; Grueneisen, A; Wambutt, R; Kalicki, J; Wohld submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25027
A;Accession: T50027
A;Accession: T50027
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A;Introns: 26/1; 74/3; 147/3
C;Superfamily: annexin I; annexin repeat homology
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A;Molecule type: DNA
A;Residues: 1-316 <BEV>
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                                                                                                              TYPEKYFEKVLRQAINKLGTDEWGLTRVVTTRAEFDMERIKEEYIRRNSVPLDRAIAKDT
                                                                                                                             TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                                                       EKAYADDDLIRILTTRSKAQISATLNHYKNNFGTSMSKYLKE
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                                                                                    RGDYEKMLVALLGEDDA 317
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Pred. No. 2.7e
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smatches 61;
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annexin P33 - maize
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 0
C;Accession: T02961
R;Battey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A;Title: CDNA isolation and gene expression of maize annexins P33
A;Reference number: Z14796; MUID:97092863; PMID:8938425
A;Accession: T02961
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-314 <BATy
A;Coss-references: UNIPROT:Q43863; EMBL:X98244; PIDN:CAA66900.1
A;Experimental source: cultivar clipper; root tip
C;Superfamily: annexin repeat homology
F;14-85/Domain: annexin repeat homology <AXR>
                                                                                                                                                          A;Cross-references: UNIPROT:Q9LX08; EMBL:AL356332; GSPDB:GN00063; A;Experimental source; cultivar Columbia; BAC clone T31P16 C;Genetics:
                                                                                                                                                                                                                                                                                                                      annexin-like protein - Arabidopsis thaliana
N;Alternate names: protein T31P16.210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50026
C;Accession: T50026
R;Bevan, M; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Kalicki, J.; Wohle submitted to the Protein Sequence Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
T50026
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A; Residues: 1-318 <BEV>
A; Cross-references: UNI
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A; Accession: T50026
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A; Introns: 26/1; 74/3; 147/3
                                                                                                                                         C;Genetics:
A;Gene: ATSP:T31P16.210
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                                                                               C;Superfamily:
                  Query Match
Best Local &
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
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  194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MATIKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MATLKVPATVPPVADDCDQLRKAFQGWGTNEALIISILGHRDAAQRRAIRRAYAEAYGEE
                                                                                 annexin I; annexin repeat homology
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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61.5%; Score 991.5;
60.8%; Pred. No. 2.60
tive 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1000.5; DB Pred. No. 6.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
2.6e-57;
tes 70;
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    Indels
                                       Length
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  Gaps
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1 MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED

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annexin P35 - maize
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02975
R;Battey, N.H.; James, N.C.; Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A;Title: CDNA isolation and gene expression of maize annexins P33 and P35.
A;Reference number: Z14796; MUID:97092863; PMID:8938425
A;Accession: T02975
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross references: UNIPROT:Q43864; EMBL:X98245; NID:g1370602; PIDN:CAA66901.1; A;Experimental source: cultivar clipper; root tip C;Superfamily: annexin I; annexin repeat homology F;14-85/Domain: annexin repeat homology <AXR>
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Best Local Similarity
Matches 185; Conserv
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                                             TRDYEDIMLALLGAE 314
                                                                                         RGDYEKMLVALLGED 315
                                                                                                                                                                                                                                KKAYSDEEIIRILTTRSKAQLLATFNSYKDQFTHAINKDL-KADPKDEFLSTLRAIIRCF
                                                                                                                                                                                                                                                                                                                            VKQAYHDRFKRSLEEDVAAHVTGDFRKLLVPLVSAYRYDGPEVNTSLAHSEAKILHEKIH 180
                                                                                                                                                                                                                                                                                                                                                                                                                     LLRALGDEIHGKFERAVILWTLDPAERDAVLANEEAKKSHPGGRALVEIACARTPAQLFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 949.5; DB 2
Pred. No. 1.4e-54;
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RESULT

12

MATIRVPNEVPSPAQDSETLKQAIRGWGTDEKAIIRVLGQRDQSQRRKIRESFREIYGKD

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probable annexin [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear Cress) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) (1990) 
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A84809
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R;Wilkinson, J.Q.; Lanahan, M.B.; Conner, T.W.; Klee, H.J.

Plant Mol. Biol. 27, 1097-1108, 1995

A;Title: Identification of mRNAs with enhanced expression

A;Reference number: S56673; MUID:95284359; PMID:7766892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487; PM A;Accession: A84809
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C;Species: Fragaria x ananassa (garden strawberry)
C;Date: 10-Oct-1995 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-321 <STO>
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A; Residues: 1-271 <WIL>
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Gene: At2g38760
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                                                                                                                                                          Matches
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Best Local
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                                                                                                                                                    124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 MTLAKQEAKLVHEKIKOKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKS-LEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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1 MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                                                                                                                                                                                                      Similarity
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                                                                                                                                               66;
                                                                                                                                                                                                Score 602.5; DB 2
Pred. No. 4.7e-32;
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Pred. No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE002093; NID:g3785996; PIDN:AAC67342.1; GSPDB:GA
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                                                                                                                                               Mismatches
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PMID:10617197
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3.5e-43;
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C; Superfamily: annexin I;
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A; Residues: 1-316 <STO>
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                                                                                                                                                                                                                                                                 1 MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                                                                                                                                  IKQVYSNTFGVKLEEDIESEASGNHKRVLLAYLNTTRYEGPEIDNASVENDARTLKSAVA
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                           AENSCFYFAKALRKSMKGLGTDDTALIRIVVTRAEVDMQFIITEYRKRYKKTLYNAVHSD
                                                                            ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                                                                                                      LRKRLHSELHGHLKKAVLLWMPEAVERDASILKRSLRGAVTDHKAIAEIICTRSGSQLRQ
                                                                                                                                                                                                               LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIFCIDTPEKHFAKVVRDSIEGFGTDEDSLTRAIVTRAEIDLMKVRGEYFNMYNTSMDNA
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                                                  LTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYORRNSIPLEKAITKD
                                                                                                      DKHYNDED-VIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQC
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A;Gene: GDB:ANXA13

A;Cross-references: GDB:9836021; OMIM:602573

A;Map position: 8g24.1-8g24.2

C;Superfamily: annexin I; annexin repeat homology

C;Keywords: blocked amino end; calcium binding; duplication; endonexin fold

F;2-316/Product: annexin intestine-specific #status experimental <MAT>

F;17-88/Domain: annexin repeat homology <AX1-

F;28-44/Region: endonexin fold #status predicted

F;89-160/Domain: annexin repeat homology <AX3-

F;100-116/Region: endonexin fold #status predicted

F;172-244/Domain: annexin repeat homology <AX3-

F;189-200/Region: endonexin fold #status predicted

F;248-316/Domain: annexin repeat homology <AX4-

F;259-275/Region: endonexin fold #status predicted

F;248-316/Domain: annexin repeat homology <AX4-

F;259-275/Region: endonexin fold #status predicted

F;2/Modified site: myristylated amino end (Gly) (in mature form) #status endonexin fold #status predicted
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J. Cell Biol. 116, 405-422, 1992
A;Title: A strategy for isolation of cDNAs encoding proteins
A;Reference number: A41733; MUID:92112982; PMID:1530946
A;Accession: A41733
A;Molecule type: mRNA
A;Molecule type: mRNA
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Search completed: August 19, Job time : 41 secs
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C;Genetics:
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Pred. No. 1.8e-25;
1; Mismatches 115
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-7621
US-09-949-016-7621
US-08-526-136-4
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US-08-526-136-13
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Sequence 62, Appl Sequence 66, Appl Sequence 66, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7952, Ap Sequence 10475, A Sequence 7621, Appli Sequence 7621, Appli Sequence 4, Appli Sequence 13, Appli Sequence 7070, Ap Sequence 7071, Ap Sequence 7071, Ap Sequence 7069, Ap Sequence 10531, Appli Sequence 10531, Appli Sequence 10531, Appli Sequence 10531, Appli Sequence 11534, Appli Sequence 1, Appli 
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	GDDDDKFLALLRSTIQCL 240	18	Length 316;  ndels 1; Gaps 1;  AEQRKVIRQAYHETYGED 60	Patent No. 5225537 Sequence 10177, A Sequence 2, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 39, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 16, Appli Sequence 16, Appli Sequence 41904, A Sequence 48004, Appli Sequence 42650, A Sequence 4980, Appli Sequence 4980, Appli

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GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

FITTLE OF INVENTION: Compositions affecting p

TITLE OF INVENTION: death and their use in t

FILE REFERENCE: 1022

CURRENT APPLICATION NUMBER: US/09/325,932A

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 206

SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity
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SOFTWARE: FastSEQ for
SEQ ID NO 66
LENGTH: 184
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/325,932A CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Pinus radiata
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TYPE: PRT
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69.6%;
                                                                                                                                                                              35.6%; Score 573; DB 4; 59.9%; Pred. No. 3.1e-48; ative 33; Mismatches 40
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Pred. No. 7.6e-77;
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Sequence 6593, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION: Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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LENGTH: 323
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Best Local Similarity
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TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSE97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
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SOFTWARE: PatentIn Vei
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OF SEQ ID NOS: 207012
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181 EQ 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 SLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIKDKHYNDED-VI 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 DFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHARQAYHARYKK 131
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Pred. No. 5.6e-38;
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; ORGANISM: Human
US-09-949-016-6593
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US-09-949-016-7952
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7952
LENGTH: 334
TYPE: PRT
                                                                                                                                                                             Query Match
Best Local Similarity
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SEQ ID NO 6593
LENGTH: 323
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Best Local
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                                                                                                    APSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGEDLLKTLDKELSN
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HFEHLMVALVTPPAVFDAKQLKKSMKGAGTNEDALIEILTTRTSRQMKDISQAYYTVYKK 149
                                   DFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHARQAYHARYKK 131
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                                                                               SPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKELKDDLKGDLSG
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                                                                                                                                                          29.3%; Score 472; DB 4; Length 334; ilarity 36.3%; Pred. No. 5.9e-38; Conservative 63; Mismatches 130; Indels
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PRIOR APPLICATION NUMBER: 60/241.755
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237.768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-10475
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US-09-949-016-10475
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TYPE: PRT
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Local Similarity 35.7%; Pred. No. 1.8e-36;
hes 112; Conservative 58; Mismatches 129;
303 DYEKMLVALLGEDD 316
                                                                                                                           608 KPLFFADKLYKSMKGAGTDEKTLTRIMVSRSEIDLLNIRREFIEKYDKSLHQAIEGDTSG
                                                                                                                                                                                                                                          243 PELYFYDYLRSAINKTGTDEGALTRIYTTRAEIDLKYIGEEYQRRNSIPLEKAITKDTRG
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RESULT 8 US-09-949-016-10476

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-10476
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7621, Applic Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                           APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL001307
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
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US-08-526-136-2
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US-09-949-016-7621
                                                     APPLICATION NUMBER: 07/837,775
APPLICATION NUMBER: 07/837,775
APPLICATION NUMBER: 07/764,465
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 00786/0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Towle, Christine TITLE OF INVENTION: ANNEXIN
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Pred. No. 1,4e-35;
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RESULT 11
US-08-526-136-4
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APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 00786/099001
TELECHMUNICATION INFORMATION:
TELEPHONE: (617) 542-8070
TELEPHONE: (617) 542-8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Towle, Christine
TITLE OF INVENTION: ANNEXIN
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: 1
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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LENGTH: 503
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ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 225 |
CITY: Boston
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                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 63
LENGTH: 111
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 63, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:
                                                                                                                                                         Query Match 27.9%; Score 449; DB 4; Length 111; Best Local Similarity 80.8%; Pred. No. 2.1e-36; Matches 84; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 27.9%; Score 450; DB 3; Best Local Similarity 36.0%; Pred. No. 1.6e-35; Matches 111; Conservative 57; Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 505
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                     134 EEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHE
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89
                                                                                                 73 FERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHARQAYHARYKKS
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                                                                            8 ORLVVLWSLDPAERDAYLANEATKRWTSSNQVLMEIACTRSPQQLLMARQAYHARYKKSL
EEDVAHHTTGDFRKLLVPLVSSYHYDGDEVNMTLAKAEAKILHE
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RESULT 13 US-08-526-136-13

Application US/08526136

Patent No. 6107089

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Best Local Similarity
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordDerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Towle, Christine TITLE OF INVENTION: ANNEXIN NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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TOPOLOGY: N/1
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LLLAIVGQ 466
                                 MLVALLGE 314
                                                                      FAERLYYAMKGAGTDDSTLVRIVVTRSEIDLVQIKQMFAQMYQKTLGTMIAGDTSGDYRR
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                                                                                                        FVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDTRGDYEK 306
                                                                                                                                          TRSFPQLRATMEAYSRMANRDLLSSVSREFSGYVESG-----LKTILQCALNRPAF
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225 Franklin Street
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRASSEQ for Windows Version 4.0
SEQ ID NO 7070
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US-09-949-016-7071
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: INFORMATION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMEER: US/09/949,016
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 7071, Application US/09949016 Patent No. 6812339
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Best Local Similarity 33.1%;
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TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 AILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLHARQAYHARYKKSLEE 135
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; SEQ ID NO 7071
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7071
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Search completed: August 19, 2005, 20:28:18 Job time : 44 secs
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                                    307 MLVALLGE 314
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460 LLLAIVGQ 467
                                                                                       247 FVDVLRSAINKTGTDEGALTRIVTTRABIDLKVIGEEYQRRNSIPLEKAITKDTRGDYEK 306
                                                                                                                  400 FAERLYYAMKGAGTDDSTLVRIVVTRSEIDLVQIKQMFAQMYQKTLGTMIAGDTSGDYRR 459
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    1611
1185.5
1177.5
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1171.5
1171.5
1132.5
1054.5
1009.5
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

20: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

21: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

22: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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73.1
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73.7
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70.3
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1 MATIKVSDSVPAPSDDAEQL.....KDTRGDYEKMLVALLGEDDA 317
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Copyright (c) 1993 - 2005 Compugen
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US-10-393-840-56

US-10-424-599-144032

US-10-425-114-97663

US-10-425-114-55802

US-10-219-220-62

US-10-393-840-114

US-10-219-220-260

US-10-424-599-21329

US-10-426-77-701-45089

US-10-425-114-60631
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Sequence 2, Appli
Sequence 144032,
Sequence 144032,
Sequence 47663, A
Sequence 55802, A
Sequence 62, Appl
Sequence 114, App
Sequence 213299,
Sequence 213299,
Sequence 45089, A
Sequence 60631, A
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<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	ü	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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0-393-840-52	-10-393-840-1	-10-219-220-6	-10-424-599-2	-10-437-963-1	-10-425-115-21396	-10-437-963-1	-10-425-114-4	-10-437-963-1	393-840-	-10-424-599-2	-10-424-599-2	0-424-599-2	-10-739-930-92	-10-425-114-43	0-425-114-55	-10-424-599-27984	-10-424-599-2303	-10-424-599-17290	-10-424-599-23142	-10-393-840-	-10-393-840-	-10-219-220-65	0-425-114-	-10-739-930-7	-10-425-115-2483	-10-767-701-4610	-10-437-963-1	5-114-4005	-10-437-963-1807	-10-425-114-5928	0-425-114-60	-10-425-114-6	-10-425-115-186
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence		Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence					Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
52, Appl	œ	•	Ξ	169441,	213961,	169438,	41196, A	121221,	55, Appl	273745,	211315,	279847	9279, A	43962,	55270, A	279849,	230318,	172904,				5, A	43123, Ā	820,	4	109	161226,	0052	9	9	0513,	27	186841,

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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10690564
Publication No. US20050089872A1
GENERAL INFORMATION:
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Best Local S
Matches 317
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CURRENT APPLICATION NUMBER: US/10/690,564
CURRENT FILING DATE: 2003-10-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: KOPATENTIN 1.71
SEQ ID NO 2
LENGTH: 317
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOREA KUMHO PETROCHEMICAL CO., I
                                                                                                                                                                          / Match 100.0%; Score 1611; DB 17; Local Similarity 100.0%; Pred. No. 1.5e-130; nes 317; Conservative 0; Mismatches 0;
121
              121 ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
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                                                                        LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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CURRENT APPLICATION UNMBER: US/10/393,840
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILING DATE: 2000-08-10
PRIOR PRIOR DATE: 1998-10-10
PRIOR PRILING DATE: 1998-10-12
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT NZ/99/00169
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 956
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 316
                                   RESULT 3
US-10-424-599-144032
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US-10-393-840-56
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US-10-393-840-56
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Sequence 144032, Application US/10424599 Publication No. US20040031072A1
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Best Local Similarity
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TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of plant Cell Wall Polysaccharides
FILE REFERENCE: 11000.1012c3
                                                                                                                            301 RGDYEKMLVALLGEDDA 317
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ilarity 71.9%;
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Pred. No. 7.8e-94;
8; Mismatches 50
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; FEATURE:
; OTHER INFORMATION: Clone ID:
US-10-425-114-47663
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                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
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APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Cap Yongwei
APPLICANT: Cap Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FULE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NO 144032
LENGTH: 316
LENGTH: 316
                                                       TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 47663
LENGTH: 333
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 47663, Application US/10425114
Publication No. US20040034888A1
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Best Local
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226; Conservative
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                    700661911_FLI.pep
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US-10-425-114-55802
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF ESQ ID NOS: 73128
SEQ ID NO 55802
LENGTH: 333
                                                                                                                                                                                                                                                                                                                        Matches
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Best Local S
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Best Local
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                                                                                                                                                                                                                                                                                                                                       Local Similarity
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NKAYNDDDFIRILATRSRAQINATLNHYKDAFGQDINKDL-KADPKDEFLSLLRATVKCL 256
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                                                                                                    ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                                                                                                   LLXTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH 120
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                                                                                  ARKAYHVLYKKSLEEDVAHHTTGDFRKLILPLVSSYRYEGDEVNLTLAKTEAKLLHEKIS
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                                                                                                                                                                                                                                                                                                                      Conservative
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Sequence 114, Application US/10393840
Publication No. US20030229922A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Cell Wall FILE REFERENCE: 11000.1012c3
CURRENT APPLICATION NUMBER: US/10/393,840
CURRENT FILING DATE: 2003-03-0
PRIOR APPLICATION NUMBER: US 09/636,800
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US-10-393-840-114
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US-10-219-220-62
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Matches
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 62
LENGTH: 316
TYPE: PRT
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APPLICANT: Lasham, Annette
ITILE OF INVENTION: Compositions affecting programmed cell
ITILE OF INVENTION: death and their use in the modification of
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
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nes 226; Conserv
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316; 1;

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plant development

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PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PCT NZ/99/00169

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 956

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 114

LENGTH: 316

TYPE: PT

ORGANISM: Pinus radiata

US-10-393-840-114
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US-10-219-220-260
; Sequence 260, App
; Publication No, 1
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                                                                                                                                   US-10-219-220-260
                                                                                                                                   APPLICANT: LASHAM, Annette

APPLICANT: LASHAM, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of plant development

FILE REFERENCE: 11000.1022c1

CURRENT APPLICATION NUMBER: US/10/219,220

CURRENT FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 290

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 260

LENGTH: 316

TYPE: PRT

ORGANISM: Eucalyptus grandis
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Best Local (
                                                                  Matches
                                                                                Query Match
Best Local Similarity
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o, US20030082724A1
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                                                                            70.3%; Score 1132.5; D 68.8%; Pred. No. 3e-89;
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RESULT 9
US-10-424-599-213299
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SEQ ID NO 213299
LENGTH: 319
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Best Local Similarity
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APPLICANT: Kovalic David
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APPLICANT: Cao Yongwei
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OTHER INFORMATION: Clone
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OTHER INFORMATION: unsure at all Xaa locations
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NAME/KEY: unsure
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ORGANISM: Glycine
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KCLTYPEKYFAKVLRLAINKLGTDEGALTRVVTTRAEVDLQRIAEEYQRRNSIPLDRAIA
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ilarity 66.8%;
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Pred. No. 1.6e-
45; Mismatches
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RESULT 11
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US-10-767-701-45089
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US-10-767-701-45089
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Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
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TITLE OF INVENTION: Nucleic Acid Molecules Associated Acid Molecu
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaeka, Jack E
APPLICANT: Tabaeka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53)31)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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LENGTH: 314
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192; Conserv
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                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 186841
LENGTH: 340
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LENGTH: 339
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                                                                                                                                                                                                                          Query Match
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Best Local 9
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
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121 ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
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                                     87 LLRSITDEISGDFERAVILWTLDFAERDAVLANEAARKWKPGNRVLVEIACTRTSAQIFA 146
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US-10-425-114-64727
; Sequence 64727, Application US/10425114
; Publication No. US20040034888A1
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Sequence 60513, Application US/10425114
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Best Local Similarity
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LENGTH: 361
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILING DATE: 2003-04-28
UNMBER OF SEQ ID NOS: 73128
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ORGANISM: Zea mays
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                                                                                                                         301 RGDYEKMLVALLGED 315
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347 SGDYESMLLALLGQE 361
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Pred. No. 1.5e-78;
53; Mismatches 70; I
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
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US-10-425-114-59289
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                                                          APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: School, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated v
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS REFERENCE: 38-21(53)31)B
FILLS REFERENCE: 38-21(53)31)B
FURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 59289
LENGTH: 344
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT FILLY APPLICATION NUMBER: US/10/425,114
CURRENT FILLYG DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 60513
LENGTH: 341
TYPE: PRT
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Publication No. US20040034888A1
GENERAL INFORMATION:
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                       TYPE: PRT
ORGANISM:
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Tabaska, Jack E
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Result
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9(2002).  Lu YP., Flav k/DDBJ databas k/DDBJ databas e J.M., Lenz C Chung M., Gon Chung M., Gon Chung M., Gon Chung M., Palm uyen M., Palm ederspiel N.A. k/DDBJ databas	Different Ara 3914) (PGR 99 A., Lam B., Carninci P. Shida J., Kam Pham P.K., Sa Yamada K., k/DDBJ databa k/DDBJ databa k/DDBJ shida	AA. update) on update) nnexin (F1 nmexin (F2 mbryophyta ions; core	
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RL Submithed (JAN-2003) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: Belongs to the annexin family.

CC -!- SIMILARITY: Contains 4 annexin repeats.

DR EMBL; AP083913; AAD43236.1; -.

DR EMBL; AV086570; AAM63633.1; -.

REMBL; AV086570; AAM63633.1; -.

REMBL; AC021198; AAF7982.1; -.

PR EMBL; AF332435; AAG48798.1; -.

PR EMBL; BT003359; AAG29977.1; -.

PR EMBL; BT003559; F:calcium ion binding; IEA.

DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.

DR GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.

DR InterPro; IPR00146; Annexin.

DR InterPro; IPR009118; Annexin.

DR PRINTS; PR0191; Annexin; 4.

DR PRINTS; PR0191; ANNEXIN; 1.

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Q39001;
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01-NOV-1996
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01-MAR-2004
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01-FEB-1997
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GO; GO:0005504; F:calcium-dependent phospholipid binding; IEA.
GO; GO:000544; F:calcium-dependent phospholipid binding; IEA.
InterPro; IPR001464; Annexin;
Pfam; PF00191; Annexin;
PRINTS; PR00196; ANNEXIN.
PRODOM; PD000143; Annexin; 4.
SMART; SM00335; ANNEXIN; 1.
RANNEXIN; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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MEDLINE=97008169; PubMed=8855345; DOI=10.1073/pnas.93.20.11268;

Gidrol X., Sabelli P.A., Fern Y.S., Kush A.K.;

"Annexin-like protein from Arabidopsis thaliana rescues delta on mutant of Escherichia coli from H2O2 stress.";

Proc. Natl. Acad. Sci. U.S.A. 93:11268-11273(1996).

-i- SIMILARITY: Belongs to the annexin family.

-i- SIMILARITY: Boongs to the annexin repeats.

EMBL; U28415; AAC49472.1; -.

EMBL; U28415; AAC49472.1; -.
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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(TrEMBLrel. 02, Last sequence update)
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NON TER
SEQUENCE
                                                                                       Brassica juncea (Leaf mustard) (Indian mustard).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Brassica.
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PRINTS; PRO1814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4
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InterPro; IPR009118; Annexin_plant.
Pfam; PP00191; Annexin; 4.
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Schantz M.L., Houlne G.;
Schantz R., Schantz M.L., Houlne G.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Gossypium hirsutum (Upland cotton).

Gusaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; eudicotyle

eurosids II; Malvales; Malvaceae; Malvo:
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C:-: SIMILARITY: Belongs to the annexin family.

C:-!- SIMILARITY: Belongs to the annexin family.

C:-!- SIMILARITY: Belongs to the annexin repeats.

R EMBL; U73746; ARB67993.2; -.

R PDB; 1N00; X-ray; A=1-315.

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0005544; F:calcium-dependent phospholipid bin R InterPro; IPR001464; Annexin.

R InterPro; IPR001464; Annexin plant.

Pfam; PF00191; Annexin; 4.

PRINTS; PR01814; ANNEXINPLANT.
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Best Local S
Matches 230
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Acala SJ-2; TISSUE-Cotton fibers;
MEDLINE-97374485; PubMed-9230934;
Delmer D.P., Potikha T.S.;
"Structures and functions of annexins in plants.";
Cell. Mol. Life Sci. 53:546-553(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyjedona; core eudicots; rosid
eurosids II Malvales; Malvaceae; Malvoideae; Gossypium.
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01-OCT-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR009118; Annexin plant. Pfam; PF00191; Annexin; 4.
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PRINTS; PR01814; ANNEXINPLANT.
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Pred. No. 2.8
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Best Local S
Matches 229
       response to low temperature.";

Plant Cell Physiol. 41:177-184 (2000).
-!- SIMILARITY: Belongs to the annexin far-
-!- SIMILARITY: Contains 4 annexin repeat.
EMBL; AF006197; AR871830.1; --
HSSP; P93157; IN00.
GO; GO:0005509; F:calcium ion binding; IE;
GO; GO:0005544; F:calcium-dependent phospl
                                                                                                                                                                                                                                                                                                                                          022341
022341;
                                                                                                                                                         TISSUE=Leaves without petioles;
Vazquez-Tello A., Uozumi T.;
"Cloning and characterization of a Lavatera thuringiaca cDNA
an annexin whose expression is stimulated by low temperature.
Plant Physiol. 0:0-0(1997).
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                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eleurosids II; Malvales; Malvaceae; Malvoideae; Lavates
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01-JAN-1998
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                                                                                            "Two novel intrinsic annexins
                                                                                                                TISSUE=Leaves without petioles; MEDLINE=20255875; PubMed=10795312;
                                                                                                                                                                                                                                                                                       Name=AnxLt1;
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                       SEQUENCE FROM N.A.
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       GO:0005509; F:calcium ion binding; IEA. GO:0005544; F:calcium-dependent phospholipid
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Pred.
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No. 1e-67;
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Best Local Sim
Matches 225;
PIR; S66274; S66274.

PDB; 1DK5; X-ray; A/B=1-314.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005504; F:calcium-dependent phospholipid |
InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin plant.

Pfam; PF00191; Annexin; 4.

PRINTS; PR00196; ANNEXIN.

PRINTS; PR01814; ANNEXINPLANT.
                                                                                                                                                                                                                                                                                           Proust J., Houlne G., Schantz M.L., So
"Characterization and gene expression
development in Capaicum annuum.";
FEBS Lett. 383:208-212(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the annexin repe EMBL; X93308; CAA63710.1; -.
                                                                                                                                                                                                                                                                                                                                           MEDLINE=96198603; PubMed=8925897; DOI=10.1016/0014-5793(96)00252-9; Proust J., Houlne G., Schantz M.L., Schantz R.; "Characterization and gene expression of an annexin during fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996
01-MAR-2004
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Capsicum annuum (Bell pepper).
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Annexin; Calcium, Calcium-binding; Calcium/phospholipid-binding;
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PRINTS; PR01814; ANNEXINPLANT.
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Pfam; PF00191; Annexin; 4.
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Pred. No. 1.9e
43; Mismatches
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Best Local S
Matches 212
    Query Match
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Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2004
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-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; AJ130829; CAA10210.1; -.
HSSP; Q42657; 1DK5.
GO: CO.nnarra
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SEQUENCE
                                                                                                                                       PRINTS; PR00196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                              GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:000554; F:calcium-dependent phospholipid
InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin plant.
Pfam; PF00191; Annexin; 4.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster

lamiids; Solanales; Solanaceae; Capsicum.
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SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Proust J., Schantz R.;
Submitted (DEC-1998) to the
                                                                                         PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4072;
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les 212; Conserv
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Last annotation update)
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Pred. No. 6.6e
58; Mismatches
    Score 1112.5;
                                                  58C69B8F0A04C0DC CRC64;
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                                                                                           Calcium/phospholipid-binding;
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Best Local S
Matches 211
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                                                                                                                                                                                                                                                                                         Repeat.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Proust J., Houlne G., Schantz M.L., Schantz R.;

Proust J., Houlne G., Schantz M.L., Schantz R.;

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Helongs to the annexin family.

-!- SIMILARITY: Contains 4 annexin repeats.

EMBL; AJ130956; CAA10261.1; -.
                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capsicum annuum (Bell pepper).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP, P93157; 1N00.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid
InterPro; IPR001464; Annexin.
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Annexin P38.
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01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00191; Annexin; 4.
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                                                                                                                                                                                                                                                                                         36138 MW;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                         Score 1109.5; DB 2; Pred. No. 2.1e-62; 7; Mismatches 58;
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RESULT 11
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                                                                                         Query Match
Best Local S
Matches 218
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P93158;
01-MAY-1997 (TrEMBLrel. 0
01-MAY-1997 (TrEMBLrel. 0
01-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                            Repeat.
                                                                                                                                                                                                                                                                         PRINTS; PR00196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
SMART; SM00335; ANNEXIN; UNK
PROSITE; PS00223; ANNEXIN; UNK
                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin_plant.
Pfam; PF00191; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U73747; AAB67994.1;
PIR; T10807; T10807
HSSP; P93157; 1N00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Physiol. 113:305-305(1997).

-!- DOMAIN: A pair of annexin repeats may form
-calcium and phospholipid (By similarity).
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Acala SJ-2; MEDLINE=97161127; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annexin (Fragment)
Name=AnnGh2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potikha T.S., Delmer D.P.; "CDNA Clones for Annexin AnnGh1 (Accession No. (Accession No. U73747) from Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gossypium hirsutum (Upland
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3635
                                                                                                                                                                                                                                                          Annexin;
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                                                                                                                  Similarity
                                  TLKVSDSVPAPSDDAE-QLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGEDL
                                                                                                                                                                                                                                                        PS00223; ANNEXIN; UNKNOWN Calcium; Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KTPEKYFEKVLRVAIKGLGTDEWDLTRVVATRAEVDMERIKEEYNKRNSVTLDRAITGDT
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TLKVPVHVPSPSEDAEWQLRKAFEGWGTNEQLIIDILAHRNAAQRNSIRKVYGEAYGEDL
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                                                                                                                                                                                      315
                                                                                            Conservative
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PubMed=9008398;
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35834 MW;
                                                                                                               69.0%;
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Last sequence update)
Last annotation updat
                                                                                         Score 1107; DB Pred. No. 3e-62; Mismatches
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_Calcium/phospholipid-binding;
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                                                                                            Indels
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                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
Repeat.
SEQUENCE 316 AA; 35937 MW; 99E7973FC04C5FBE CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster
lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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InterPro; IPR009118; Annexin plant.
Pfam; PF00191; Annexin; 4.
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01-NOV-1999 (TrEMBLrel. 12,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XEN8;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vacuole-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XEN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                       MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAEQRKVIRQAYHETYGED
                            ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVMTLAKQEAKLVHEKIK 180
                                                                                                                                LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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                                                                                                                                                                                             MASLKVPTSVPEPYEDAEQLKKAFAGWGTNEALIIQILAHRNAAQRKLIRETYAAAYGED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPEQYFEKVLRQAINKLGSDEWALTRVVTTRAEVDMVRIKEAYQRRNSIPLEQAIAKDTS
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ARQAYHARYKKSLEEDVAYHTTGDFRKLLVPLLTAFRYEGEEANMTLARKEANI LHEKI S
                                                                                            LLKDLDAELTSDFORAVLLWTLSPAERDAYLVNEATKRLTSSNWVILEIACTRSSDDLFK
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                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                Score 1106.5; DB Pred. No. 3.3e-62;
                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                Query Match
Best Local S
Matches 208
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O24131;
O1-JAN-1998
                                                                                                                                                                                                                           GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005544; F:calcium-dependent phospholipid binding; IEA.
GO; GO:000544; F:calcium-dependent phospholipid binding; IEA.
InterPro; IPR001464; Annexin,
Pfam; PF00191; Annexin; 4.
PRINTS; PR00196; ANNEXIN; 1.
PRINTS; PR01814; ANNEXIN; A.
PRODOM; PD000143; ANNEXIN; 4.
SMART; SM00335; ANN; 4.
PROSITE; PS00223; ANNEXIN; 1.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                Repeat.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Nicotiana.
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05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=X511; Synonyms=an.1;
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                                                                                                                                                                           Similarity
DKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
                                              ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK
                                                                            LIKELDRELTNDFEKLVVVWTLDPSERDAYLAKEATKRWTKSNFVLVETACTRSPKELVL
                                                                                      LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
                                                                                                                     RGDYEKMIVALLGEDDA 317
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                                                                                                                                                                                                          314 AA;
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                                                                                                                                                                 Conservative
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                                                                                                                                                                                                           35855 MW;
                                                                                                                                                                          68.1%;
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                                  /AYHTTGEHPQLLVPLVSSYRYGGDEVDLRLAKAEAKILHEKIS
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                                                                                                                                                                Score 1096.5;
Pred. No. 1.4e
59; Mismatches
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edons; core eudicots; aster
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Best Local (
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SEQUENCE
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-i-SIMILARITY: Belongs to the annexin family.
-i-SIMILARITY: Contains 4 annexin repeats.
EMBL; AJ401032; CAB92956.1; -.
HSSP; Q42657; 1DK5.
G0; G0:0005509; F:calcium ion binding; IEA.
G0; G0:0005544; F:calcium-dependent phospholipid binding;
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PRINTS; PR00196; ANNEXIN.

PRINTS; PR01814; ANNEXINPLANT.

PRODOM; PD000143; Annexin; 4.

SMART; SM00335; ANX; 4.

PROSITE; PS00223; ANNEXIN; 1.

Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster lamiids; Solanales; Solanaceae; Solanum.
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01-MAR-2004
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001464; Annexin.
InterPro; IPR009118; Annexin_plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum (Potato)
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                                                                                                                                                                                                           DKHYNDEDVIRILGTRSKAQINATFNRYQDDHGEEILKSLEEGDDDDKFLALLRSTIQCL
                                                                                                                                                                                                                                                                                                                      ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                       LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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                                                                             VYPEHYFVEVLRDAINRRGTEEDHLSRVIATRAEVDLKTIANEYQKRDSIPLGRAIAKDT
                                                                                                     TRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLKVIGEEYQRRNSIPLEKAITKDT
                                                                                                                                                                   DKAYSDDEVIRILATRSKAQLNATLNHYKDEYGEDILKQLE-
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Last sequence update)
Last annotation update)
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Pred. No. 1.4e-61;
6; Mismatches 47
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O81536;
O1-NOV-1998
O1-NOV-1998
O1-MAR-2004
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Repeat.
SEQUENCE
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GO; GO:0005544; F:calcium-dependent phospholipid binding;
InterPro; IPR0011464; Annexin.
InterPro; IPR00118; Annexin.
Pfam; PF00191; Annexin; 4.
PRINTS; PR00196; ANNEXIN.
PRINTS; PR01814; ANNEXINPLANT.
PRODOM; PD000143; ANNEXINPLANT.
PRODOM; PD000143; ANNEXINPLANT.
PRODOM; PR000143; ANNEXINPLANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lim E.-K., Roberts M.R., Bowles D.J.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: Belongs to the annexin family.
-!- SIMILARITY: Contains 4 annexin repeats.
EMBL; AF079232; AAC97494.1; -.
HSSP; Q42657; IDX5.
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Eukaryota; Viridiplantae; Strepchyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster.

lamiids; Solanales; Solanaceae; Solanum.
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Lim E.K., Roberts M.R., Bowles D.
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                                                                                                                                                   ARQAYHARYKKSLEEDVAHHTTGDFRKLLVSLVTSYRYEGDEVNMTLAKQEAKLVHEKIK 180
                                                                                                                                                                                                                                                                                                                                                                                               LLKTLDKELSNDFERAILLWTLEPGERDALLANEATKRWTSSNQVLMEVACTRTSTQLLH
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  RGDYEKMLVALLGEDD
                                                  VYPEHYFVEVLRDAINRRGTEEDHLTRVIATRAEVDLKTIANEYQKRDSVPLGRAIAKDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35801 MW; 18A7A50886A60AFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%;
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7; Mismatches
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Search completed: August 19, 2005, 20:46:32 Job time : 182 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USTO_spool/US10690564/runat 19082005 172307 25292/app_query.fasta_1.455
-Q-/cgn2 1/USTO_spool/US10690564/runat 19082005 172307 25292/app_query.fasta_1.455
-DB=GenEmbl -QFMT=fastap -SUFFIX-rige -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLENO -MAXLEN-2000000000
-USER=US10690564 @CGN_1 1 3731 @runat 19082005 172307 25292 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG SCORES=0 -WAIT -DSTBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                            Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                      Score
    1611
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                                                                     Match
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Ygapop 10.0 , y
Fgapop 6.0 , E
Delop 6.0 , E
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Copyright (c) 1993 - 2005 Compugen Ltd.
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## ALIGNMENTS

rerectic ormitation.	Score:	Pred. No.:	alignment co	ORIGIN		source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	CQ806050
	1244	Č H						CropDesig	Patent: 1	Identific	Inze,D.,	_	rosids;	Spermato	Eukaryot	Arabidop	Arabidop	•	CQ806050	CQ806050	Sequence	CQ806050	
	1611.00	8.28e-129		/db_xref="taxon:3702"	/organism="Arabidopsis thaliana" /mol_type="unassigned DNA"	1. 954	Location/Qualifiers	CropDesign N.V. (BE)	Patent: WO 2004035798-A 2461 29-APR-2004;	Identification of novel e2f target genes and use thereof	<pre>Inze,D., de Veylder,L. and Vlieghe,K.</pre>		rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Arabidopsis thaliana	Arabidopsis thaliana (thale cress)		CQ806050.1 GI:47111659		Sequence 2461 from Patent WO2004035798.		
COMBCT AGCT AC.	Matches:	Length:		3702"	dopers charran signed DNA"		ers		461 29-APR-20	2f target gene	nd Vlieghe, K.		sicales; Brası	nyta; eudicoty	Streptophyta		le cress)				: WO2004035798	954 bp DNA	
:	317	954			18."	•			)4;	es and use the			sicaceae; Arab	ledons; core e	<pre>; Embryophyta;</pre>						•	linear	
										reof			idopsis.	udicots;	Tracheophyta;							PAT 10-MAY-2004	

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Arabidopsis thaliana (thale Cress, Arabidopsis, Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Core eudicots, Spermatophyta, Magnoliophyta, eudicotyledons, Core eudicots, Spermatophyta, Magnoliophyta, Erassicales, Brassicaceae, Arabidopsis, Coreids, eurosids, I; Brassicales, Brassicaceae, Arabidopsis, Coreids, Eurosids, Eurosids, Eurosids, Eurosids, Eurosids, Eurosids, Eurosids, Eurosids, Eurosids, European, Eur
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Submitted (28-DEC-2000) Plant
Submitted (28-DEC-2000) VSA
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3 (bases 1 to 954)
Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Quach, H.L.,
Yamada, K., Dale, J.M., Hsuan, V.W., Onodera, C.S., Chen, H., Cheuk, R.
Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R.
Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A
Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-MAY-2003) Plant Gene Expression Street, Albany, CA 94710, USA Annotation based on July 2002 version of the F submitted to Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Etgu,I
Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Chen,H.,
Kariin-Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M.,
Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis, A.
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DEVNNTLAKORAKLYHEKIKJKHYNDEDVIR.ILSTRSKAGINATFNRYQDDHGEBIL
SLEEGDDDDKFLALLRSTIQCLTRPELYFYDVLRSAINKTGTDEGALTRIVTTRAEID
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it was in pUNI-T3-D/V5-His-TOPO under the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
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/product="putative Ca2
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                                                                                                                                                                                                           GAAGAGGAGTACCAGCGCAGGAACAGCATTCCTTTGGAGAAAGCTATTACCAAAGACACT
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ORGANISM
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Conservative: Mismatches: Indels: Gaps:

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Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAs: Nguyen, M., Tripp, M., Southwick, A., Palm, C.J., Jones, T., Wu, T., Cheuk, R., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V.W., Lee, J.M., Kim, C.J., Quach, H.L., Onodera, C.S., Shinn, P., Tang, C.C., Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; 'RIKEN Arabidopsis Full-Length cDNA'); Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Submitted (29-JAN-2003) DNA Sequencing and Technology
Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Southwick, A., Nguyen, M., Tripp, M., Palm, C.J., Jones, T., Wu, T Carninci, P., Chen, H., Cheuk, R., Chan, M.M., Chang, C.H., Dale, Deng, J.M., Hayashizaki, Y., Hsuan, V.W., Lee, J.M., Ishida, J., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Onodera, C.S., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Shinn, P., Tang, C. Toroumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinoataki, K., Ecker, J., Theologis, A. and Davis, R.W.
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Arabidopsis thaliana (thale cress)
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
roside; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="At1g35720"
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 thaliana (thale cress)
                                GI:21405280
                                                            thaliana clone
                                                              25846 mRNA,
                                                              complete sequence
                                                                              linear
                                                                            PLN 14-APR-2003
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ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis

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1 (bases 1 to 1192)

1 (bases 1 to 1192)

Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Feldmann,K.A., Flavell,R.B., Sequences greatly improve genome
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Brover, V., Troukhan, M.,
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DEVNWTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATENRYQDDHGEEILK
SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAKTGTDEGALTRIVTTRAEID
SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAKTGTDEGALTRIVTTRAEID
                                                                                                                                                                                                                                                     LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
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/mol_type="mRNA"
/db_xref="taxon:3702"
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,B., Miranda,M.,

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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1208 bp Arabidopsis thaliana Ca2+-dependent annexin (At1g35720) mRNA, complete
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Submitted (02-JAN-2002) DNA Sequencing and Technology
Stanford University, 855 California Avenue, Palo Alto,
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/protein_id="AAL61954.1"
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Clark, G.B. and Roux, S.J.
Isolation and Characterization of Two Different Arabidopsis cDNAs (Accession Nos. AF083913 and AF083914) (PGR 99-065)
Plant Physiol. 120 (1), 340 (1999)
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Clark, G.B. and Roux, S.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetAlaThrLeuLygValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
AspLysHisTyrAsnAspGluAspValIleArgIleLeuSerThrArgSerLysAlaGln
                                                      AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys
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                                     GATGAAGTGAACATTGGCTAAGCAAGAAGCTAAGCTGGTCCATGAGAAAATCAAG
                                                                                                             ACTACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTGTTACCTCATACAGGTACGAAGGA
                                                                                                                                ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                                                                                                                                 GCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCAC
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Austin, TX 78713, USA
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SLEEGDDDDKFLALLASTIQCLTREBLYFVDVLRSALNKTGTDEGALTRIVTTRAEID
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/mol_type="mRNA"
/cultivar="Columbia"
/db_xref="taxon:3702"
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Submitted (06-JUN-1995) Anil K. Kush, Institute of Molecular & Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Republic of Singapore
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1159)
1 (bases 1 to 1159)
Gidrol,X., Sabelli,P.A., Fern,Y.S. and Kush,A.K.
Annexin-like protein from Arabidopsis thaliana rescues delta oxyR mutant of Escherichia coli from H2O2 stress
Proc. Natl. Acad. Sci. U.S.A. 93 (20), 11268-11273 (1996)
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                                                                                                                                                                                           /varTety="ecotype Columbia"
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                                                                                                                          note="annexin-like protein"
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ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla
                           GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
                                                                               AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValIle
                                                                                                                                                     ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
                                                                                                                                                                                            GAGGAAGGAGATGATGACAAGTTGCCTTGCACTTTGAGGTCAACCATTCAGTGCTTG
                                                                                                                                                                                                           GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu
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 LysThrLeuAspLysGluLeuSerAsnAspPheGluArgAlaIleLeuLeuTrpThrLeu
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/db_xref="G1:1429207"
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EEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEIDLK
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/mol_type="mRNA"
/sub_species="ecotype Columbia"
/db_xref="taxon:3702"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica
Jami, S.K. and Kirti, P.B.
Direct Submission
Submitted (30-JUL-2003) Department of Plant
Life Sciences, University of Hyderabad, Gach
Andhra Pradesh 500046, India
Location/Qualifiers
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Jami,S.K. and Kirti,P.
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   GluGluGlyAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu
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SLEEGDEDDKFLGLLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVATRAEID
LKVIGQEYQRRNSIPLEKAITKDTRGDYEKMLIALLGEDDA"
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                                                                                                                     Submitted (28-JUN-2000) Plant Gene Expression Center, 800 Buchanan St., Albany, CA 94710, USA
On Feb 11, 2000 this sequence version replaced gi:6693723.
The sequence is of BAC F14D7 from Arabidopsis thallana chromosome
1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 6954 by because we submit only the unique sequence of the clone. However, in order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide small overlaps (200 bp) between overlapping sumbitted clones. The 5' end of this sequence overlaps by 200 bp to the 3' end of the sequence of the clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 81513)

Liu, S.X., Chan, A., Sakano, H., Yu, G., Lee, J.M., Lenz, C., Pham, P., Toriumi, M., Chin, C., Chiou, J., Choi, B., Lee, J.M., Gonzalez, A., Howng, B., Liu, A., Vaysberg, M., Altafi, H., Brooks, S., Buehler, E., Chao, Q., Conn, L., Conway, A.B., Hansen, N.F., Johnson-Hopson, C., Khan, S., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R., Federspiel, N.A., Theologis, A. and Yu, G.

The sequence of BAC F14D7 from Arabidopsis thallana chromosome 1
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-FEB-2000) P
Street, Albany, CA 94710,
4 (bases 1 to 81513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Street, Albany, CA 94
3 (bases 1 to 81513)
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Arabidopsis thaliana
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                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / CTAILS ALL COLD - GALO - GAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF 00191. ES'
gb N96455, gb
gb R30014, gb
gb H36260, gb
gb H76134, gb
gb AA597533, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gi 7267527 fr
gb AL161513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (join (7937. .8041,8115. 8757. .8919,9397. .10730))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7937. .10730)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLEEGDDDDKFLALLRSTIQCLTRPELYFVDVLRSAINKTGTDEGALTRIVTTRAEID
LKVIGEEYQRRNSIPLEKAITKDTRGDYEKMLVALLGEDDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MATLKVSDSVPAPSDDAEQLRTAFEGWGTNEDLIISILAHRSAE
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DEVNWTLAKQEAKLVHEKIKDKHYNDEDVIRILSTRSKAQINATFNRYQDDHGEEILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thaliana gb AF083913
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MKVTEKCDVYSFGVLILELIIGKHPGDLVSSLSSSPGEALSLRSISDERVLEPRGQNR
EKLLKMVEMALLCLQANPESRPTMLSISTTFS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Contains similarity to a putative protein CAB78009
91|7267527 from Arabidopsis thaliana BAC T32A17
gb|AL161513. It contains Pumilio-family RNA binding
domains PF|00806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F14D7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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misc_feature
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DALISSIMFEGNNRVSQTLAAMEASRGFYPEEDSSILSFFHEKVSKLGASYLEDTVL
IGQGSYGKMSPKSNNDLVSMYEIYGSVNLMAKDQIGCRVLQKLVEEGTFHEAKVILLA
IIDHYVELSMDPFGNYIVQKLFDVSDEEQRTLIVSVLTSNPRELLTRICLMTYGTRVQ
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CAEIAIHRHGCCVLQCCISNSVGLQRERLVAEISRNSLHLSQDPFGNYVVQYLIDQDY
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TCPWRVYATKLPDSDWFEVRSTTQTHTCSVDARGDFHKQASTVVIGKLMRTKYIGVGR
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// gene "F14D7,5"

complement (join(34011. .34115,34201. .34450,34532. .34788,34873. .35035,35279. .36183))

// gene = "F14D7,5"

// note = "Contains similarity to a putative RNA-binding protein AAF18550 gi| 6587864 from Arabidopsis thaliana BAC T11111 gb|AC012680. It contains Pumilio-family RNA binding domains PF| 00806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="meifnfqqasdhrrlpdfgsggflqsldtnpflknqyynnsvea
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/gene="F14D7.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(19422. .19496,19746. .19835,20053. .20194,
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gene

SdC

SGS

gene

gg

314

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeuValThr 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACTTTTAAACATCTTGTGTGAAGTCATTGTATTCTAATTGGTTTTTTGGTCATGGACAG 6820
                                        IleAspLeuLysValIleGlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLys
                                                                                                                                                               TCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCA
                                                                                                                                                                                  SerThrIleGlnCysLeuThrArgProGluLeuTyrPheValAspValLeuArgSerAla
                                                                                                                                                                                                                                    GAAATTCTCAAGAGTCTTGAGGAAGGAGGATGATGACGACAAGTTCCTTGCACTTTTGAGG
                                                                                                                                                                                                                                                            GluIleLeuLysSerLeuGluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArg
                                                                                                                                                                                                                                                                                                                               ThrArgSerLysAlaGlnIleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGlu
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                                                                                                                                                                                                                                                                                                                                                                                                    ValHisGluLysIleLysAspLysHisTyrAsnAspGluAspVallleArgIleLeuSer 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerTyrArgTyrGluGlyAspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeu 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGACGTTGCTCACCACACTACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTTGTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerThrGlnLeuLeuHisAlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGlu 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThrArgThr 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGCTATCTTGTTGGACTCTTGAACCCCGGTGAGCGTGATGCTTTATTGGCTAATGAA 6880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgAlaIleLeuLeuTrpThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACAGAGGAAAGTCATCAGGCAAGCATACCACGAAAACCTACGGCGAAGACCTTCTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluGlnArgLysValIleArgGlnAlaTyrHisGluThrTyrGlyGluAspLeuLeuLys 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleAsnLysThrGlyThrAspGluGlyAlaLeuThrArgIleValThrThrArgAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTOTTGACAAGGAGOTOTOTAACGATTTOGA-GGTTCGGTTTTCGGACTTTTAAGTATO 6760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPRANELRRMLRQDYALIQPYFKCLLETNPNSLVAMETEKDNSGVERFKYLFFALDAC
VQGYAYMRKVIVIDGTHLRGRYGGCLVAASAQDANFQVFPIAFGIVNSKNDEAWTWFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.23e-112
1450.00
90.40$
90.40$
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Gossypium hirsutum
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Eusermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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/COGON Start=1
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/protein_id="AAC33305.1"
/protein_id="AAC33305.1"
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EGVNMMLAKTERKLLHEKISDKAYSDDDVIRVLATNSKAQINATLNHYKNEYGNDINK
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/db_xref="taxon:3635"
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Potikha, T.S. and Delmer, D.P.
Direct Submission
Submitted (09-OCT-1996) Plant Sciences, Hebrew University,
Submitted (09-OCT-1996) Plant Sciences, Hebrew University, Hebr
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Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Malvaceae; Malvoideae; Gossypium.
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Structures and functions of annexins
Cell, Mol. Life Sci. 53 (6), 546-553
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                         Campus, Jerusalem 91904, Israel
Aug 20, 2001 this sequence version replaced gi:1843524
Location/Qualifiers
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                                               ACTGGGGACTTCCATAAGCTCCTCCTACCTCTAGTGAGTTCATACAGATATGAGGGAGAG
                                                                           ThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGlyAsp
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/db xref="G1:15214410"
/db xref="G1:15214410"
/translation="A71TVPTTVPSVSEDCEQLRKAFSGWGTNEGLIIDILGHRNAEQ
RNLIRKTYAETYGEDLLKALDKELSNDFERLVLLWALDPAERDALLANEATKRWTSSN
QVLMEIACTRSANQLLHARQAYHARYKKSLEEDVAHTTGDFEKLLLLEUVSSYRYEE
EVNMTLAKTBAKLLHEKGISNRAYSDDDVIRYLATRSKAQINATLNHYKNEYGWDIKKD
LKADPKDEFLALLRSTVKCLVYPEKYFEKVLRLAINRRGTDEGALTRVVCTRAEVDLK
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/tissue_type="cotton
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Alignment : Pred. No.: Score:	ORIGIN	FEATURES source			Comment	JOURNAL	REFERENCE AUTHORS TITLE	SOURCE	ACCESSION VERSION	RESULT 13 BD236006 LOCUS DEFINITION	D Qy	B &	B &	B 8	da VQ	B &	Db 4	OV B
Scores: 7.55e-92 Length: 2588 1185.50 Matches: 228	/mort_rype= yerrountc unn /db_xref="taxon:71139"	Location/Qualifiers  12588 //organism="Eucalptus grandis" //organism="Eucalptus grandis"	dification of plant cell wal alifiers	ONARD NATHAN BLOKSBERG C12N15/09, A01H5/00, C12N5/10, C12N9/00, C12N9/12, C12N15/00, C1	PN JP 2002527056-A/28 PN JP 2002527056-A/28 PD 27-AUG-2002 PD 27-AUG-2002 PD 27-AUG-2002 PD 08-CCT-1999 JP 2000575985 PF 08-CCT-1999 IP 2001575985	cent: JP 2002527056-A 28 27-AUG-2002; NESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER RESTS LTD	9.6		6		302 GlyAspTyrGluLysMetLeuValAlaLeuLeuGly 313                :::   :::            898 GGAGACTATGAAAAATTGCTGCTGCTACTTGCAGGA 933	282 GluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThrArg 301	262 GluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAepLeuLySValIleGly 281	242 ArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThrAsp 261	222 GluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeuThr 241	202 AsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIlcLeuLysSerLeuGlu 221	AAAGCTTACAGTGATGACGATGTCATAAGGGTTTTGGCTACAAGAAGCAAGGCACAGATC	
SULT 14 006197	Qy 301 ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla 317	Qy 281 GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr 300	Qy 261 ASpGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLy8ValIle 280	Qy 241 ThrargProGluLeuTyrPheValAspValLeuArgSerAlaileAspLysThrGlyThr 260	Qy 221 GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu 240 :::	Qy 201 IleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGluGluIleLeuLysSerLeu 220	Qy 181 AspLysHisTyrAsnAspQdluAspValIleArgIleLeuSerThrArgSerLysAlaGln 200	Qy 161 AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys 180	Qy 141 ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly 160		Qy 101 SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis 120	Qy 81 ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr 100 :::   :::	Oy 61 LeuLeuLysThrLeuAspLysGluLeuSsrAsnAspPheGluArgAlaIleLeuLeuTrp 80              :::        :::	Qy 41 ArgSerAlaGluGlnArgLysVallleArgGlnAlaTyrHisGluThrTyrGlyGluAsp 60    :::          :::	Qy 21 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis 40	Qy 1 MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu 20    :::              :::               1390 ATGTCGACTCTCACCGTCCCGCAGCCACTGCCCCTGTAGCCGATGACTGCGAGCACTC 1449	10-690-564-2 (1-317) x BD236006 (1-2	Percent Similarity: 83.91% Conservative: 38  Best Local Similarity: 71.92% Mismatches: 50  Query Match: 73.59% Indels: 1  DB. 6

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Vazques-Tello,A. and Uozumi,T.
Cloning and characterization of a Lavatera thuringiaca
Cloning and characterization of a Lavatera thuringiaca
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Lavatera.
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1 (bases 1 to 1112)
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Submitted (31-MAY-1997) Biological Sciences, Universite du Quebec,
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Breton,G., Vazquez-Tello,A., Danyluk,J.
Two novel intrinsic annexins accumulate
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 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
                                                                   MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
                                                    ATGGCTACTCTTACAGTTCCCTCCACACTTCCGTCAGTGTCTGAAGATTGTGAACAACTC
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                                                                                                                                                                                                                                                                                                              /product="annexin"
/protein_id="AAB71830.1"
/protein_id="AAB71830.1"
/db_xref="qci:2459926"
/translation="MATLITVPSTLPSVSEDCEQLRKAFSGWGINEDL1INILGHRNAD
/translation="MATLITVPSTLPSVSEDCEQLRKAFSGWGINEDLLINILGHRNAD
/translation="MATLITVPSTLPSVSEDCEQLRKALDPERDALLANEATKRWTSS
NOVIMEIACRSSSDQLLRARQAYHVRYKKSLEEDVAHTTTGDFRKLLLPLVSSYRYEG
DEVNWTLAKTERKLLHEKISNKAYSDDDVIRVLATRSKSQINERLNYKNEYATDINK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="AnxLt1"
/function="binds acidic phospholipids in a calcium-dependent manner"
/note="calcium-dependent, phospholipid binding protein; contains four characteristic repeats found in both anim
                                                                                                                                                                                                                                                                                                 KI IADBYQRRNSVPLTRAIVKDTNGDYEKLLLVLAGEVEA"
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/tissue_type="leaves without
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 1293)
Bloksberg, L.N.
Materials and method for modification of plant cell w
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Pinus radiata (Monterey pine)
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GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE PORESTS LTD
OS Pinus radiata (radiata pine)
PN JP 2002527056-A/56
PD 27-AUG-2002
PF 08-OCT-1999 UP 2000575985
PR 13-OCT-1998 US 09/170862,11-AUG-1999 US 60/148426 PI LEONARD NATHAN BLOKESBERG
PC C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/12,C12N15/00,C12N5/PC 00
CC Materials and method for modification of plant cell wall CC
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                                                                                              ACAACTGGAGATTTTCGTAAGTTGCTGGTACCTCTTGGGAGCTCCTACCGTAATGATGGA
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/mol_type="genomic DNA"
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ACTGGAGACTATGAAAAAATGCTTCTGGCATTGATTGGCCACGTCGAGGCT
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Search completed: August 22, 2005, 11:53:31
Job time : 4984 secs

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Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-Q-/cgn2 1/USPTO_sp.model -DEV=xlh
-Q-/cgn2 1/USPTO_spcol/US10690564/runat 19082005 172306 25282/app query.fasta_1.455
-Q-/cgn2 1/USPTO_spcol/US10690564/runat 19082005 172306 25282/app query.fasta_1.455
-DB- Q=neseq_16Dec04 -QFMT-fasta_D -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER-US10690564 @CGN 1.1 470 @xrunat 19082005 172306 25282 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aaf44757 Annexin-l	AAF4		٧	20
Aaa67129 Pinus rad	AAA67			20
Aaa67096 Pinus rad	AAA670	704 3	34.9	563
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Aaf44760 Annexin-l	<b>AAF447</b>		5	573
Aaa67132 Pinus rad			5	573
Aac42551 Arabidops			7.	2
Aac45661 Arabidops	AAC45661		7.	602.5
Abz14750 Arabidops			7.	2
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Acn53624 Cotton an			0	659
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Cotton			5	738
Adr63464 Cotton cD			46.1	742
Aaa67099 Pinus rad	٠.		7.	757.5
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Acn60265 Cotton gy			48.1	775
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Adr63461 Cotton cD	3 ADF	184	74.6	٠

## ALIGNMENTS

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ADJ63871 standard; DNA; 954 BP.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel isolated lipid metabolism proteins (LMP) and encoding nucleic acids comprising a polymucleotide sequence encoding a polypeptide that functions as a modulator of seed storage compounds in a plant. The LMP nucleic acid is useful in producing transgenic plants with increased levels of seed storage compound, e.g. lipid, a fatty acid, a starch or a seed storage protein, as markers for specific regions of the genome and for evolutionary and protein structural studies. The present sequence represents an LMP nucleic acid of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d metabolism proteins and nucleic acids, useful ic plants with increased levels of seed storage fatty acid, a starch or a seed storage protein.
GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
                       AspLysHisTyrAsnAspGluAspVallleArgIleLeuSerThrArgSerLysAlaGln
                                                                   AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys
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                                                                                                             ACTACCGGTGACTTCAGAAAGCTTTTGGTTTCTCTTGTTACCTCATACAGGTACGAAGGA
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; ss; plant; transgenic; E2Fa/DPa transcription growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon
                                                                                                                                                                                                                             Altering plant characteristics, useful for producing plants for enzyme pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                     Claim
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P-PSDB; ADN74567.
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                                                ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
                                                                                                          GAGGAAGGAGATGATGACAAGTTCCTTGCACTTTTGAGGTCAACCATTCAGTGCTTG
                                                                                                                                     GluGluGlyAspAspAspAspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeu
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                            ACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGTTCAGCAATCAACAAAACTGGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance;
                                                                                                                                             07-MAY-2001; 2001US-00849529
12-DEC-2001; 2001US-00021323
  Kovalic
                                              (KOVA/)
(ZHOU/)
(CAOY/)
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WPI; 2004-667718/65

New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).

Claim 1; SEQ ID NO 4242; 14pp; English

the 58798 Cotton plant CDNA sequences mentioned in the specification.

C Also a recombinant polypeptide comprising any of the 58798 amino acid

C sequences mentioned in the specification and producing a plant having an

C improved property. Producing a plant having an improved property

C comprises transforming a plant with a recombinant construct comprising a

C promoter region functional in a plant cell operably joined to a

C promoter region functional in a plant cell operably joined to a

C polynuclectide comprising a coding sequence for a polypeptide associated

C polynuclectide comprising a coding sequence for a polypeptide associated

C plant cells by modification of the cell cycle pathway, improving plant

C plant cells by modification of the cell cycle pathway, improving

C plant tolerance, providing increased resistance to plant disease,

C producing galactomannan (or lignin or plant growth regulators), improving

C plant heat tolerance, improving plant tolerance to herbicides, increasing

C the rate of homologous recombination in plants, improving plant tolerance

C to extreme osmotic conditions or to pathogens or peste, improving yield

C and/or content, improving yield by modification of carbohydrate, nitrogen

C plant growth and development under at least one stress condition. The

C polynuclectide and polypeptide may also be used in recombinant DNA

C constructs, in physical arrays of molecules, as plant breeding markers,

C or in computer-based storage and analysis systems. The present sequence

C seqdata.uspto.gov/sequence.thml?Doc.10=20040181830. However only 6585

C polynuclectide sequence were available, the remaining 52213

C polynuclectides and all 58798 protein sequences were not present. invention relates to a recombinant polynucleotide comprising any of

Sequence 1184 BP; 375 A; 233 C; 281 G; 295 7; 0 U; 0 Other;

Query Best Local Percent Similarity: Match: Similarity: 6.07e-112 1202.50 15.30\$ 73.48\$ 74.64\$ Matches: Conservative: Mismatches: Indels: Gaps: 1184 230 37 45 1

US-10-690-564-2 (1-317) x ADR63461 (1-1184)

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                                                                 ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr
                                                                                                          CTCCTCAAGGCACTAGACAAGGAGCTCTCGAATGACTTTGAGAGGCTGGTTTTGCTTTGG
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences given in Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16288 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the Claim 1; Page 48-49; 301pp; English New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant. P-PSDB; AAB16294. present invention of to

Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-10-690-564-2 (1-317) 8.78e-110 1185.50 83.91% 71.92% 73.59% x AAA67100 (1-2588)Length:
Matches:
Conservative:
Mismatches:
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ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr TCCTCAAGGCATTGGACAGAGAACTTACCAATGATTTCGAGAGGCTGGTGGTCCTTTGG LeuLeuLysThrLeuAspLysGluLeuSerAsnAspPheGluArgAlaIleLeuLeuTrp AGGAATGCGGCGCAGAGGAAGCTGATTCGGCAAACCTATGCCGAGACTTACGGCGAGGAC ArgSerAlaGluGlnArgLysVallleArgGlnAlaTyrHisGluThrTyrGlyGluAsp CGGACAGCCTTCGCAGGATGGGGAACAAATGAGAAGCTGATCATATCCATATTGGGTCAT ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu ACAACTGGAGATTTTCGTAAGTTGCTGGTACCTCTTGTGAGCTCCTACCGTTATGATGGA TCACTTGATCCGGCTGAACGTGATGCGTACTTGGCGAATGAAGCGGAAAAGATGGACT TCAAGCAACCAGGTTCTAATGGAAATAGCCTGCACGAGGTCTCCGCAGCAGTTGCTTATG 140 120 100 1929 1809 1689 1629 1569 1449 180 160 1509 08 60 40 20

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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polypaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polypaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are
                                                                                                                                                                                                                                                                                                                                            New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated polynucleotide (I) comprising a nucleotide sequence that is one of 145 fully defined sequences of 221-3415 base pairs (bp), given in the specification, and/or its complements, reverse complements, reverse sequences, or sequences having 75, 90 or 95 sequence identity to or that hybridise under stringent hybridisation conditions to one of the 145 sequences. The methods and compositions of the present invention to do with (I) are useful for modulating programmed cell death and thereby altering the development cycle of plant cells, and altering plant development. This sequence encodes a protein associated with the programmed cell death pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide useful for modulating programmed cell death, altering the development cycle of plant cells, and subsequently modifying plant development.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1293
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                                                                                                                                                                                     AGGAATGCGGCGCAGAGGAAGCTGATTCGGCAAACCTATGCCGAGACTTACGGCGAGGAC
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programmed cell death; plant development; plant cell cycle; ATL2; DAD1; Dnase; lls; lsd1; nucellin-like aspartic protease; annexin; prohibitin; fen-like protein; rac2; retinoblastoma-related protein; SINA; TFIID; TEGT; xylogenic Rnase; pur-alpha; cyteine protease; RPP5-like protein; gp 91 NADPH oxidase subunit; NPR-like protein; BAG-l; defender against cell death; lethal leaf spot; lesion stimulating death, seven in absentinia; transcription initiation factor;
                                                                                                                     04-JUN-1999;
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CTTAATGCAACCCTCAATTACTACAACAATGAGTTTGGGAATGCCATCAACAAGGATCTG
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The present invention describes a method for identifying and validating plant genes/proteins as targets for agrochemicals comprising determining the gene or protein expression profiles of a plant and downregulating the expression of the gene or protein in the plant or plant cell. Also described: (1) methods for screening candidate agrochemical compounds, comprising the use of the above method or the use of any of the 785 fully defined nucleotide sequences (ADF37942 to ADF38726) or protein sequences, or their homologues, functional fragments or derivatives; (2) a method for producing an agrochemical resistant plant, comprising the use of the above-mentioned nucleotide or protein sequences; (3) an isolated nucleotic acid that is identified by any of the above methods or that comprises at least a part of a nucleic acid sequence chosen from any of the 785 culled that is identified by any of the above methods or that comprises at nucleotide sequences given in the specification; (4) a plant tolerant to an agrochemical, in which the expression level of one or more of the culled acid sequences given in the specification is modulated; and (5) a harvestable part of the plant described above. The method is useful in cidentifying and validating plant targets for agrochemicals or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying and validating plant genes or proteins as targets for agrochemicals, useful for producing agrochemical-resistant plants, comprises determining and down regulating the gene or protein expreprofiles of a plant.
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CC This invention relates to a novel method for altering one or more plant CC characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric CC E2Fa/DPa transcription factor of Arabidoppis and using these sequences to CC generating transgenic plants for the production of growth regulators, CC enzymes, therapeutics, pharmaceuticals and animal feed products, where CC the altered plant characteristics are selected from increased yield or CC biomass, enhanced survival capacity, stress tolerance, plant architecture CC or physiology, altered endoreduplication, biochemistry, signal CC transduction, storage lipid mobilisation and/or altered photosynthesis, CC each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers CC during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polymucleotide sequence is thate cress cDNA repressed 1.3 fold or more in plants overexpressing the E2Fa/DPa transcription factor, given in an exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; ss; plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism
Sequence
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                ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
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RESULT 15 AAC40038 ID AAC40038 ID AAC40038; XX AC40038; XX DT 17-OCT-2000 (first entry) XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 26820. XX WHybridisation assay; genetic mapping; gene expression control; XX WHybridisation assay; senetic mapping; gene expression control; XX WHYDIS TOWN PROMOTER; termination sequence; ss. XX OS Arabidopsis thaliana. XX OS Arabidopsis thaliana. EP1033405-A2.	815 ÁCÁTACCCTCÁGAAGCÁTTTTGAGAAGGTTCTTCCGTCTATCAÁCÁÁAATGGÁÁATACCÁTÁCÁÁAATGGÁÁÁCÁ 874  261 ASPGIUGIYAIALEUTHTATGIIEVAITHTTHTATGAIGIUIIEASPLEULYSVAIIIE 280	TGAACATGATGCTTGCAAGATCTGAAGCTAA TGAACATGATGCTTGCAAGATCTGAAGCTAA TGAACATGATGCTTGCAAGATCTGAAGCTAA TGAACATGATGCTTACAGATCTTCATCAGAATCTT  AGTICAGTGACGATGACTTCATCAGAATCTT  AGTICAGTGACCACTACAACAACGAGTATGG  AGTICAGACCACTACAACAACGAGTATGG  AGTICAGACAATGACTACAACAACTACTACTACTACAACGACGACAATGACTACTACAACGAGTATGGS  AGTICAGACAATGACAATGAAACTACTACTACTACTACTACTACTACTACTACTACTAC	::             :::        ACGCAGCACAACCGCAGCTTGATCCGCAGCGTTT ACGCAGCACCAACCGCAGCTTGATCCGCAGCGTTT 
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                                  AspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuValHisGluLysIleLys 180
                                                                                                                                           GATGATGTGAACATGATGCTTGCAAGATCTGAAGCTAAGATACTTCACGAGAAGGTCTCA
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-/Ggn2_1/USPTO_spool/US10690564/runat 19082005 172307 25304/app_query.fasta_1.455
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANGS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10690564 @CGN 1 1 3437 @TUNAT 19082005 172307 25304 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG-SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BX841810 Arabidops
CF652924 B5-LO2013
BX838972 BX838972
CF652048 30-LO2058
CA782049 011E11AF
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## ALIGNMENTS

COMMENT	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	AUTHORS TITLE	VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 CNSOABR2 LOCUS DEFINITION ACCESSION
- web: www.genoscope.cns.rr) The sequences are based on single pass reads.  Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.  Genoscope members carried out sequencing and annotation: Castelli v., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,	Unpublished 2 (bases 1 to 1095) 2 (bases 1 to 1095) Genoscope. Direct Submission Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : By 1 91006 EVRY Cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  A Combined Approach to Evaluate and Improve Arabidopsis Genome	BX816579.1 GI:42471684 HTC; GSLT cDNA. Arabidopsīs thaliana (thale cress) Arabidopsīs thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosides; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 105)	CNSOABR2  1095 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPCH56ZG07 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).

FEATURES

300 862

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Percent Similarity:
Best Local Similarity:
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URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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/tissue_type="Hormone 1
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGY INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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1 (castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Chachter, V., Wenard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Weissenbach, J. and Salanoubat, M. Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
Whole Genome Sequence Comparisons and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNSOABTJ
Arabidopsis thaliana Full-length CDNA Complete sequence GSITPEH18ZF02 of Hormone Treated Callus of strain col-0 Arabidopsis thaliana (thale cress)
                                                                                                                                                                                          http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
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1. .1137
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                                                                                                      LeuArgSerThrIleGlnCysLeuThrArgProGluLeuTyrPheValAspValLeuArg
                                                                                                                                                      GlyGluGluIleLeuLysSerLeuGluGluGlyAspAspAspAspLysPheLeuAlaLeu
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                                                                                          TTGAGGTCAACCATTCAGTGCTTGACAAGACCAGAGCTTTACTTTGTCGATGTTCTTCGT
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 GCTGAGATTGAACTTGAAGGTCATTGGAGAGGAGGTACCAGCGCAGGAACAGCATTCCTTTG
                                            GTTACCTCATACAGGTACGAAGGAGATGAAGTGAACATGACATTGGCTAAGCAAGAAGCT
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RESULT 3
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                                                                                  Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

UROV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Pull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1155)
1 (bases 1 to 1155)
1 (Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Castelli, V., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
Mhole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
Machine Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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HTC; GSLT_cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                          /strain="Col-0"
/db xref="taxon:3702"
/clone="GSLTSIL62E066"
/tlssue_type="Silique"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis
/mol_type="mRNA"
                                                                                                                                                                                                                                      /gene="At1g35720"
                                            1.9e-174
1561.00
98.43%
97.48%
96.90%
x CNS0AB51 (1-1155)
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RESULT 4
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                                                  1034 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS23ZB01 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
Arabidopsis thaliana
                                    BX841810.1 GI:42454468
                                                                                                                                                                                                                                                                                                                                                                  GATGAAGGAGCACTCACTAGAATTGTGACCACAAGAGCTGAAATTAACTTGAAGGTCCAT
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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1 (bases 1 to 1034)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Menard, M., Cruaud, C., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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                ThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAlaThrLysArgTrpThr
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Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thal Genome Res. 13 (6), 1250-1257 (2003)
                                                  Contact: Weisshaar B
ADIS DNA core facility at MPIZ
AMAX-Planck-Institute for Plant Breeding
Carl-von-Linne Weg 10, 50829 Koeln, Gern
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                                        ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                                                                                                                     SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis
                                                                                                                                                                                                                                                                                                                           GCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCAC
                                                                                                                   AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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//lab_host="E. coli TOP10"
//clone lib="MPIZ-ADIS-066"
//note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: Not1;
//note="Vector: pCMVSPORT6; Site_1: Site_2: Not1;
//note="Vector: pCMVSPORT6; Site_2: Not1;
//note="Vector: pCMVSPORT6; Site_2: Not1;
//note= salI-concector: plants light/day; library
//note= saliable from RZPD; contact RZPD (clone@rzpd.de)
//note= saliable from RZPD; contact RZPD (clone@rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="root"
/lab_host="E. coli 7
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Conservative:
Mismatches:
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RESULT 5 CF652924 LOCUS

DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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TITLE AUTHORS

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497 160 437 140 377 120

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JOURNAL MEDLINE PUBMED

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                                                                                                                       source
                                                                                                                                                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Costelli V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Castelli V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Castelli V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Castelli V., Schachter, V., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salannoubat, M. Temple, G., Caboche, M., Weissenbach, J. and Salannoubat, M. Weissenbach, J. and Salannoubat, M. Sequences: Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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BX838972
thaliana
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                   http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/EST
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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Unpublished (2004)
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/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="GSLTFB50ZD03"
/tissue_type="Flowers a
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Arabidopsis thaliana Flowers and buds Col-0 Arabidopsis
cDNA clone GSLTFB50ZD03 5PRIM, mRNA sequence.
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                                                                            _type="mRNA"
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schmid, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.

Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 843 Std Error: 0
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30-L020580-066-004-L08-SP6P MPIZ-ADIS-066 Arabidopsis thaliana cDNA clone MPIZp2001L084Q 5-PRIME, mRNA sequence.
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Plate: 4 row: L
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                                                                                                                                                                                                                                                                           Wassilewskija-0; roots from three weeks old plants grown on MS-plates at 26M-0C with 16 hours light/day; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites Sall-NotI, primer sites and orientation:

SP6-Sall-CCACGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; GATEWAY compatible; Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity.

'Establishment of methods for genome-wide mutation and development of methods for genome-wide mutation detection, PI: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de This clone is available from RZPD, contact RZPD (clone@rzpd.de) for further information."
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/clone_lib="Tector: pCMVSPORT6; Site_1: SalI; Site_2: Not1;
/cDNA_library_from_Arabidopsis_thaliana, accession
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tosida; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
and Welinder,K.G.
                                                                                                                                                                                                                                                              sequence.
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Ünpublished (2002)
Contact: Karen G. Welinder
Institut for bioteknologi
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Infected Arabidopsis
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bp mRNA linear EST 03-DEC-2002 s Leaf Arabidopsis thaliana cDNA, mRNA

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261 AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAsp
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GATGAAGGAGCACTCACTAGAATTGTCACCACAAGAGCTGAGATTGAC
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Sohngaardsholmsvej 4
Tel: +45 96358467
Fax: +45 98141808
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                                                                                       AspLysHisTyrAsnAspGluAspValIleArgIleLeuSerThrArgSerLysAlaGln
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                                                                                                                                                                                                                                                                            GCTAGGCAAGCTTACCATGCTCGCTACAAGAAGTCTCTTGAAGAGGACGTTGCTCACCAC
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   ATCAATGCTACTTTTAACCGTTACCAAGATGATCATGGCGAGGAAATTCTCAAGAGTCTT
                                                                     GACAAGCACTACAATGATGAGGATGTTATTAGAATCTTGTCCACAAGAAGCAAAGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
library of Arabidopsis and E. cichoracearum infected
from three weeks old Arabidopsis plants. Plants were
harvested 3 days after infection and mRNA oligo dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /ecotype="Columbia"
/db_xref="taxon:3702"
/dev_stage="Plant 3 w
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/mol_type="mRNA"
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ne_lib="Infected Arabidopsis Leaf"
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VERSION
KEYWORDS
SOURCE
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Best Local Similarity:
Query Match:
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                                                                     No.:
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                                                                                                                                                                                                                                                                                                                                                        The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              966 bp mRNA linear HTC Arabidopsis thaliana Full-length cDNA Complete sequence GSLTPGH18ZH06 of Hormone Treated Callus of strain col-0 Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-NOV-2003) Genoscope
BP 191 91006 EVRY cedex - FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Arabidopsis thaliana
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                                                                                                                                                                   "mol_type="mbNA"
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/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                            organism="Arabidopsis
9.68e-147
1327.00
99.62%
99.24%
82.37%
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              Length:
Matches:
Conservative:
Mismatches:
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(E-mail : segref@genoscope.cns.f)
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DB:

Wilson, I.,

Somerville,

Denmark

infection"

leaf

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RESULT 10
BU635010
LOCUS
                                                       SOURCE
ORGANISM
                                                                                    KEYWORDS
                                                                                                         VERSION
                                                                                                                       ACCESSION
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                                                                                   sequence.
BU635010
BU635010.1
EST.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                     BU635010
003A04 Infected
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Fax: +45 98141808
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Sohngaardsholmsvej (
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Institut for bioteknologi
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EST sequencing of Erysiphe
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                                                                                      ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                                                                                                        AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
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Location/Qualifiers
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/db xref="taxon:3702"
/dev_stage="Plant 3 weeks old, three days post infect
/dev_stage="Plant 3 weeks old, three days post infect
/clone lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
/ibrary of Arabidopsis and E. cichoracearum infected
from three weeks old Arabidopsis plants. Plants were
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Institut for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg,
Tel: +45 96358467
Fax: +45 98141808
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1 (bases 1 to 775)

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Engineering
College of Life Sciences,
Beijing 100871, China
                                                                                                                             1 (bases 1 to 929)

Ji,S.J., Lu,Y.C., Feng,J.X., Wei,G., Li,J., Shi,Y.H., Fu,Q.,

Liu,D., Luc,J.C. and Zhu,Y.X.

Isolation and analyses of genes preferentially expressed during early cotton fiber development by subtractive FCR and cDNA array Nucleic Acids Res. 31 (10), 2534-2543 (2003)
                                                                                                                                                                                                                               Gossypium hirsutum (upland cotton)
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Gossypium hirsutum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; endicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Toside; euroside II; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                       Contact: Zhu,Y.
National Laboratory of Protein Engineering and
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/cultivar="Xu-142"
/db_xref="fibar"
/tissue_type="fibar"
/dev_stage="10 days post anthesis (dpa)"
/clone_lib="Cotton fiber subtracted cDNA library"
/note="The library was constructed using PCR-select cDNA
subtraction method with 10 dpa cotton fiber as tester and
fiberless mutant as driver"
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Malvaceae; Malvoideae; Gossypium.
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Plate: 03 row: B column: 10.
Location/Qualifiers
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Fax: 520 621 1259
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The University of Arizona
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Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,'
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C.
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/cnote="Vector: pCMV.SPORT-6.1; Site_1: Not1; Site_2:
/cnote="Vector: pCMV.SPORT-6.1; Site_1: Not1; Site_2:
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/dev_stage="_3 to +3 |
/lab_host="DH10B"
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/mol_type="mRNA"
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REFERENCE
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ON GR Eb28E08.r GR Eb Gossypium raimondii cDNA clone GR E CO129429

N CO129429

CO129429.1 GI:48878407

EST.

Gossypium raimondii
SM Gossypium raimondii
SM Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Wagnollophyta; eudicotyledons; core eudicorosids; eurosids; eurosids; I; Malvales; Malvaceae; Malvoideae; Gos

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Stum, D.,
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Global assembly of Cot
Unpublished (2004)
Contact: Rod A. Wing
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Fax: 520 621 1259
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GCTCTTGATCCTGCTGAACGTGATGCCCTTTTTGGCTAATGAAGCCACCAAAAAGGTGGACT
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/clone_lib="GR _Eb"
/clone_lib="GR _Eb"
/clone="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
/note="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
/scoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."
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RB019H11.r GR Eb Gossypium raimondii cDNA clone GR Eb019H11

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CO116938.1 GI:48815625

SET.

Gossypium raimondii

Gossypium raimondii

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magmoliophyta; eudicoty; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

E 1 (bases 1 to 881)

Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C., Widall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
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/clone="GR_Eb019H11"
/tissue_type="floral"
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-DB=_Issued_Patents_NA -QFMT=fastap_-SUPF/Ix=rni -MINMATCH=0.1 -LOOPCCL-0
-LOOPCLT=0 -UNITS=bite -STRATE=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCALICN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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Ygapext
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                   US-09-325-932A-17

US-09-325-932A-20

US-09-325-932A-18

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US-09-949-016-722

US-09-949-016-4604

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US-09-949-016-1750

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Sequence 17, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 18, Appl
Sequence 1149, App
Sequence 722, App
Sequence 722, App
Sequence 4604, Ap
Sequence 4605, Ap
Sequence 1750, Ap
Sequence 1750, Ap
Sequence 1, Appli
Sequence 3, Appli
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## ALIGNMENTS

US-09-325-932A-17

Sequence 17, Application US/09325932A Patent No. 6451604 GENERAL INFORMATION:

RESULT 1

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 17
LENGTH: 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
FILE REFERENCE: 1022
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                           No.:
21 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
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                                                                              1 MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
                                                           ATGTCGACTCTCACCGTCCCGCAGCCACTGCCCCCTGTAGCCGATGACTGCGAGCAGCTC
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1171.50
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71.29%
72.72%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 20, Application US/09325932A
Patent No. 6431604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITILE OF INVENTION: Compositions affecting profittle of INVENTION: death and their use in the FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
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US-09-325-932A-20
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 US-09-325-932A-21
Sequence 21, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
FILE REFERENCE: 1022
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TYPE: DNA
ORGANISM: Pinus
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; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 21
; EEQ ID NO 21
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-21
Sequence 18, Application US/09325932A
PATCENT NO. 6451604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
ITILE OF INVENTION: Compositions affecting pr
ITILE OF INVENTION: death and their use in th
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT APPLICATION STATE OF ONCE OF ONC
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RESULT 5
US-09-949-016-2081
CURRENT APPLICATION NUMBER: US/09/949,01
; CURRENT FILING DATE: 2000-04-14
; CURRENT FILING DATE: 2000-10-41,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.
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; SEQ ID NO 18
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Pinus 1
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOW
TITLE OF INVENTION: WITH HUMAN DISEASE,
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                            Sequence 2081, Application US/09949016 Patent No. 6812339
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US-09-949-016-2081
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                                                    TCCAGATCAGAAATTGACCTTTTGGACATTCGAACAGAGTTCAAGAAGCATTATGGCTAT
                                                                                                                       CTGCATCGAGCCTTGAAGGGTATTGGAACTGATGAGTTTACTCTGAACCGAATAATGGTG
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US-09-023-655-1149
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Pred. No.:
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US-09-023-655-1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for W1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS: INCYTE PH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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AAAATGCTCATCAGCATTCTGACTGAGAGGTCAAATGCACAGCGGCAGCTGATTGTTAAG
                            AspLeuIleIleSerIleLeuAlaHisArgSerAlaGluGlnArgLysValIleArgGln
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RESULT 7
US-09-949-016-722
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

FILE REFERENCE: CL001307

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/337,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-722
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 722
LENGTH: 1339
           878
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101 AGCCCATCAGTGGATGCTGAAGCTATTCAGAAAGCAATCAGAGGAATTGGAACTGATGAG
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                                   ThrArgAlaGluIleAspLeuLysVallleGlyGluGluTyrGlnArgArgAsnSerIle
                                                                                                                                                                                                                                                                                                                 GAGATCCTGTGTTTAAGGAGCTTTCCTCAATTAAAACTAACATTTGAATAAAATACAGAAAT
                                                                                                                                                              GACTTACTGTTGGCCATAGTTAATTGTGTGAGGAACACGCCGGCCTTTTTAGCCGAAAGA
         TCCAGATCAGAAATTGACCTTTTGGACATTCGAACAGAGTTCAAGAAGCATTATGGCTAT
                                                                                     CTGCATCGAGCCTTGAAGGGTATTGGAACTGATGAGTTTACTCTGAACCGAATAATGGTG
                                                                                                           LeuArgSerAlaIleAsnLysThrGlyThrAspGluGlyAlaLeuThrArgIleValThr
                                                                                                                                                                                              AlaLeuLeuArgSerThrIleGlnCysLeuThrArgProGluLeuTyrPheValAspVal
                                                                                                                                                                                                                                      ATCAGCCAAAAGGACATTGTGGACAGCATA---AAAGGAGAATTATCTGGGCATTTTGAA
                                                                                                                                                                                                                                                                        AspHisGlyGluGluIleLeuLysSerLeuGluGluGlyAspAspAspAspLysPheLeu
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472.00
56.86%
36.27%
29.30%
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Conservative:
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Gaps:
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Best Local Similarity:
Query Match:
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US-09-949-016-4604
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR TILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4604
LENGTH: 2386
TYPE: DNA
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Patent No. 6812339
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                                                                                                                                                                                                                          1358 AAGAAGGCCATGGAGGGAGCCGGCACAGATGAAAAGGCTCTTATTGAAATCCTGGCCACT
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ValThrSerTyrArgTyrGluGlyAspGluValAsnMetThrLeuAlaLysGlnGluAla 172
                                                                                                                                                                                                                                                                                                                 CTGGCAAGGCTGATTCTGGGGCTCATGATGCCACCGGCCCATTACGATGCCAAGCAGTTG 1357
                                                                                                                                                                                                                                                                                                                                                                                                      TTCAAGTCTCACTTTĠĠĊCGGĠĠĠĊŤŤAATGACTGACĊŤĠAAGTCTĠĀĠATCŤĊŤGGĀĠĀĊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAATCATCGATATCATCACGCACCGCAGCAATGTCCCAGCGGCAGCAGATCCCGGCAGACC 1237
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                                                                                                                                     CGGACCAATGCTGAAATCCGGGCCATCAATGAGGCCTATAAGGAGGACTATCACAAGTCC 1477
                                                                                                                                                                            ArgThrSerThrGlnLeuLeuHisAlaArgGlnAlaTyrHisAlaArgTyrLysLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrHisGluThrTyrGlyGluAspLeuLeuLysThrLeuAspLysGluLeuSerAsnAsp
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                                             CTGGAGGATGCTCTGAGCTCAGACACATCTGGCCACTTCAGGAGGATCCTCATTTCTCTG
                                                                                     LeuGluGluAspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeu
                                                                                                                                                                                                                                                                   AsnGluAlaThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThr 112
                                                                                                                                                                                                                                                                                                                                                        PheGluArgAlaIleLeuLeuTrpThrLeuGluProGlyGluArgAspAlaLeuLeuAla
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461.50
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35.67%
28.65%
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Matches:
Conservative:
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Indels:
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OF DETECTION AND USES THEREOF
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                                                                                                                                                          Best Local Similarity:
Query Match:
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                                                                                         US-10-690-564-2 (1-317)
                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-4605
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 4605
LENGTH: 2386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR PHILING DATE: 2000-10-03
PRIOR PHILING DATE: 2000-10-03
PRIOR PHILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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    1118 CCTGACGCAGATGCCAAAGCGCTGCGGAAAGCCATGAAGGGACTCGGGACTGACGAAGAC 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThrAspGlu
                           13 ProSerAspAspAlaGluGlnLeuArgThrAlaPheGluGlyTrpGlyThrAsnGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGACTCTGACCAGGATCATGGTATCCCGCAGTGAGATTGACCTGCTCAACATCCGGAGG
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CAGGAGTTCATCAAGATGACCAACTATGACGTGGAGCACCACCATCAAGAAGGAGATGTCT
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RESULT 10
US-09-949-016-1750
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
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LENGTH: 1932
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                                                 US-10-690-564-2 (1-317) x US-08-526-136-1 (1-2305)
                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
                                                                                                                                                                                                                                                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLIN TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: ISM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Towle, Christine TITLE OF INVENTION: ANNEXIN
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 1
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                                                                                                                                                                        No.:
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                                                                                                                                                                                                                                                                            TYPE:
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CLASSIFICATION: 435
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                                                                                                                  Sequence 3, Application US/08526136 Patent No. 6107089
                                                                                  GENERAL INFORMATION: APPLICANT: Towle,
                             NUMBER OF SEQUENCES: 3
                                                             TITLE OF INVENTION: ANNEXIN
   STREET:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,062
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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LeuGluGluAspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeu 152
                                                                                                                        AsnGluAlaThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThr 112
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                                        US-10-690-564-2 (1-317) x US-09-949-016-1199 (1-2054)
                                                                                                         Query Match:
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US-09-949-016-1199
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G.
TITLE OF INVENTION: WITH HUMAN DISEASE, MET
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241.755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             SEQ ID NO 1199
LENGTH: 2054
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SOFTWARE: FastSEQ for
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                                                                                                                                                                                                                                                                                              TYPE: DNA
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                Sequence 1200, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SEQ ID NO 1200
LENGTH: 2054
TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  566 GATGTGGTCGACCGTTCCAATGATCAGAGGCAAAAAATTAAAGCAGCATTTAAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 ThrTyrGlyGluAspLeuLeuLysThrLeuAspLysGluLeuSerAsnAspPheGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 SerIleLeuAlaHisArgSerAlaGluGlnArgLysValIleArgGlnAlaTyrHisGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspValAlaHisHisThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGAAATCCGAGAAATTGTCAGATGTTATCAGTCAGAATTTGGACGAGACCTTGAAAAG
                                                                                   GACTIGITAAGCAGTGTGAGCCGTGAGTTTTCCGGATATGTAGAAAGTGGT
                                                                                                                     GluIleLeuLysSer--------LeuGluGluGlyAspAspAsp
                                                                                                                                                                                                                                                             HisGluLysIleLysAspLysHisTyrAsnAspGluAspValIleArg---IleLeuSer 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCAGGGAGCAGGAACTCAGGAACGTGTATTGATTGAGATTTTGTGCACAAGAACAAAT
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                                                                                                                                                       ACAAGAAGCTTTCCTCAGCTGAGAGCTACCATGGAGGCTTATTCTAGGATGGCTAATCGA 1105
                                                                                                                                                                                                                          TATCAAGCTGGTGAGGGAGACTAGGGACCGATGAATCTTGCTTTAACATGATCCTTGCC
                                                                                                                                                                                                                                                                                               AATCGTGATGAGAACCAGAGTATAAACCACCAAATGGCTCAGGAAGATGCTCAGCGTCTC
                                                                                                                                                                                                                                                                                                                               TyrArgTyrGluGlyAspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuVal 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeuThrArgProGluLeuTyr 246
                                                                                                                                                                                      ThrArgSerLysAlaGlnIleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGlu
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1197
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Patent No. 6612339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CLOO1307
CURRENT ADDITOR
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                                                                                                                                                       76 AlalleLeuLeuTrpThrLeuGluProGlyGluArgAspAlaLeuLeuAlaAsnGluAla
                                                                                                                                                                                                                16
ThrGlnLeuLeuHisAlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGlu 135
                                                                                                                                                                                                                                                                                                                                                             AspAlaGluGlnLeuArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIle
                                                        ATGCAGGGAGCAGGAACTCAGGAACGTGTATTGAGTTGAGATTTTGTGCACAAGAACAAT
                                                                          ThrLysArgTrpThrSerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSer 115
                                                                                                                        CTGATCCTGGCCCTCTTCATGCCTCCTACGTATTACGATGCCTGGAGCTTACGGAAAGCA
                                                                                                                                                                                              TCCTATGGCAAGGATTTAATCAAAGATCTCAAATCAGAGTTAAGTGGAAATATGGAAGAA
                                                                                                                                                                                                                                                                                                  SerIleLeuAlaHisArgSerAlaGluGlnArgLysValIleArgGlnAlaTyrHisGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTCTTCTGGCTATTGTGGGCCAG 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgIleValThrThrArgAlaGluIleAspLeuLysValIleGlyGluGluTyrGlnArg 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGCTGAGAGGCTCTACTATGCTATGAAAGGTGCTGGCACAGATGACTCCACCCTGGTC 1258
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                                         307 MetLeuValAlaLeuLeuGlyGlu 314
                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 GluIleLeuLyaSer--------LeuGluGluGlyAspAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 ThrArgSerLysAlaGlnIleAsnAlaThrPheAsnArgTyrGlnAspAspHisGlyGlu 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 TyrArgTyrGluGlyAspGluValAsnMetThrLeuAlaLysGlnGluAlaLysLeuVal 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 AspValAlaH1sH1sThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         872 CAGGAAATCCGAGAAATTGTCAGATGTTATCAGTCAGAATTTGGACGAGACCTTGAAAAAG
CTTCTTCTGGCTATTGTGGGCCAG 1468
                                                                                                                  ArgAsnSerIleProLeuGluLysAlaIleThrLysAspThrArgGlyAspTyrGluLys 306
                                                                                                                                                                  CGGATTGTGGTCACTCGAAGTGAGATTGACCTTGTACAATAAAACAGATGTTCGCTCAG
                                                                                                                                                                                               ArgIleValThrThrArgAlaGluIleAspLeuLysValIleGlyGluGluTyrGlnArg
                                                                                                                                                                                                                                                                              PheValAspValLeuArgSerAlaIleAsnLysThrGlyThrAspGluGlyAlaLeuThr
                                                                                                                                                                                                                                                                                                                                       -----TTGAAGACCATCTTGCAGTGTGCCCTGAACCGCCCTGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                 AspLysPheLeuAlaLeuLeuArgSerThrIleGlnCysLeuThrArgProGluLeuTyr 246
                                                                                                                                                                                                                                                                                                                                                                                                                         GACTTGTTAAGCAGTGTGAGCCGTGAGTTTTCCCGGATATGTAGAAAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisGluLysIleLysAspLysHisTyrAsnAspGluAspVallleArg---IleLeuSer 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATCGTGATGAGAACCAGAGTATAAACCACCAAATGGCTCAGGAAGATGCTCAGCGTCTC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACATTAGGTCAGATACATCAGGACATTTTGAACGTTTACTTGTGTCCATGTGCCAGGGA
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Search completed: August 22, Job time : 275 secs 2005, 13:00:16

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Minimum
Maximum
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-Q=/cgn2 1/USPTO_spool/US10690564/runat_19082005_172309_25406/app_query.fasta_1.455
-DB=PublIshed_Applications_NA -CPMT=fastap -SUPFTX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=2000000000 -USER=US10654 @GCN 1 1 480 @runat 19082005 172309_25406
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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-MODEL=frame+_p2n.model
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seq length: 2000000000
Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*

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9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*

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17: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

20: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

21: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

22: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

23: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

24: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

25: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*

26: /cgn2_6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-10-690-564-1 ; Sequence 1, Application US/10690564 ; Publication No. US20050089872A1 APPLICANT: KOREA KUMHO PETROCHEMICAL CO., LTD
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ANNEXINS FROM PLANTS
FILE REFERENCE:

ALIGNMENTS

GENERAL INFORMATION:

NUMBER OF SEQ ID NOS: 4 SOFTWARE: KOPATENTIN 1.71 SEQ ID NO 1 LENGTH: 1230 TYPE: DNA CURRENT APPLICATION NUMBER: US/10/690,564
CURRENT FILING DATE: 2003-10-23 ORGANISM: Arabidopsis thaliana

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                                                                       AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValIle
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Matches:
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US-10-767-795-4242
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPERBNCE: 38-21(5354)1B CURRENT APPLICATION NUMBER: US/10/767,795 CURRENT FILING DATE: 2004-01-30 NUMBER OF SEQ ID NO.S: 117596 SEQ ID NO.4242 LENGTH: 1184 TYPE: DNA ORGANISM: Gossypium hirsutum FEATURE: TRECOMMETTING COLUMBER OF SEQ ID NO.S: 117596 ORGANISM: Gossypium hirsutum FEATURE: DNA ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4242, Application US/10767795
publication No. US20040181830A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
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73.48%
74.64%
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Conservative:
Mismatches:
Indels:
Gaps:
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APPLICANT: Bloksberg, Leonard N.

APPLICANT: Bloksberg, Leonard N.

TITLE OF INVENTION: Materials and Methods for the

TITLE OF INVENTION: Modification of Plant Cell Wall Polysaccharides

FILE REFERENCE: 11000.1012c3

CURRENT APPLICATION NUMBER: US/10/393,840

CURRENT FILING DATE: 2003-03-20

PRIOR APPLICATION NUMBER: US 09/636,800

PRIOR APPLICATION NUMBER: US 09/170,862

PRIOR FILING DATE: 1998-10-13

PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: US 60/148,426

PRIOR APPLICATION NUMBER: PCT NZ/99/00169

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 956

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 2588
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                                                  GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                   NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 7439
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Publication No. US20040034888A1
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GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cac, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
INMBER OF SEQ ID NOS: 73128
SEQ ID NO 29928
LENGTH: 1145
TYPE: DNA
ORGANISM: Glycine max
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Best Local Similarity:
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ACAACAGGAGACTTCCGTAAGCTCATACTACCTCTGGTTAGTTCTTATCGATATGAAGGA
                    ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
                                                                       GCGAGGAAGGCTTACCATGTTCTTTATAAGAAGTCTCTGGAGGAGGATGTTGCTCATCAC
                                                                                          AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis
                                                                                                                                             TCAAGCAATCAGGTTCTGGGAAATAGCCTGCACTAGGTCCTCTGAACAATTGTTTGCT
                                                                                                                                                            SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis
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RESULT 6
US-10-424-599-1190
; Sequence 1190, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE CAO TIVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 1190
LENGTH: 1393
                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max FEATURE:
OTHER INFORMATION: Clone
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                 ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
                                                                                MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
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                                                            ATGGCGACACTTAAGGTTCCTCAGCCTCTTCCCCCCGTTGCAGATGATTGTGAGCAGCTC
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      APPLICANT: Flinn, Barry
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting proj
TITLE OF INVENTION: Compositions diffecting proj
TITLE OF INVENTION: Compositions use in the
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US200300827
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
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; ORGANISM: Pinus
US-10-219-220-17
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GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLysAlaIleThrLysAspThr
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CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 09/636,800
PRIOR FILING DATE: 2000-08-10
PRIOR PILING DATE: 1998-10-13
PRIOR PILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR APPLICATION NUMBER: US 60/148,426
PRIOR FILING DATE: 1999-08-11
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 956
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LENGTH: 1293
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Publication No. US20030229922A1
GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
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ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly 160
                                                                                                                                                                              TCACTTGATCCGGCTGAACGTGATGCGTACTTGGCGAATGAAGCGACGAAAAGATGGACT
                                                                                                          TCAAGCAACCAGGTTCTCATGGAAATAGCCTGCACGAGGTCTCCGCAGCAGTTGCTTATG
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Pred. No.:
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; TYPE: DNA
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 218
LENGTH: 1058
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                                                                                                                                                                                                                                                                                                                               APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
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ArgThrAlaPheGluGlyTrpGlyThrAsnGluAspLeuIleIleSerIleLeuAlaHis
                                          ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAspAspAla
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                                                                                                                                       Sequence 10772, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
           APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
TIPLETT AND NUMBER 110
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; OTHER INFORMATION:
US-10-425-114-10772
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NUMBER OF SEQ ID NOS:
SEQ ID NO 10772
LENGTH: 1145
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hrAspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValI
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Query Match:
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US-10-424-599-70457

IS Sequence 70457, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 70457

LENCTH: 1321
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                                                                            AlaArgGlnAlaTyrHisAlaArgTyrLysLysSerLeuGluGluAspValAlaHisHis 140
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                                                                                                                                                                            SerSerAsnGlnValLeuMetGluValAlaCysThrArgThrSerThrGlnLeuLeuHis
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; SOFTWARE: FASTSEQ for W
; SEQ ID NO 655
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Arabidopsis t
US-09-770-149-655
                                                                                APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Patrick
TITLE OF INVENTION: Expressed Sequences of
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
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Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
Yu, Yang
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GACACTTCTGGAGACTATCAGAGCATTCTCCTTGCACTGGTTGGACATGAGGAT 1043
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Rameaka, Joshua G.
Page, Amy
Matthew, Abraham V.
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US-10-767-701-13525

US-10-767-701-13525, Application US/10767701

Sequence 13525, Application US-10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:
   APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated (TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT APPLICATION NUMBER: US/10/767,701

; SEQ ID NO 13525

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Pred. No.:
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LENGTH: 1385 TYPE: DNA ORGANISM: Sorghum bicolor

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; OTHER INFORMATION:
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GlyGluGluTyrGlnArgArgAsnSerIleProLeuGluLy8AlaIleThrLy8AspThr
                                             ---AAGGCTGACCCCAAGGATGAGTACCTCAAAACACTGCGGGCAATCATCCGGTGCTTC
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                                                                                           AGTTGCCCCGACAGGTACTTTGAGAAGGTCGCCAGGCCATAGCGGGGCTAGGCACA
                                                                                                               ThrArgProGluLeuTyrPheValAspValLeuArgSerAlaIleAsnLysThrGlyThr
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US-10-425-114-21986
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
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SEQ ID NO 21986
LENGTH: 1235
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Publication No. US20040034888A1
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ORGANISM: Zea mays
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                       ThrThrGlyAspPheArgLysLeuLeuValSerLeuValThrSerTyrArgTyrGluGly
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Query Match:
DB:
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FEATURE:
OTHER INFORMATION: Clone
US-10-425-114-26803
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GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(5313)B
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26803
LENGTH: 1285
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                                                                         MetAlaThrLeuLysValSerAspSerValProAlaProSerAspAspAlaGluGlnLeu
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ArgGlyAspTyrGluLysMetLeuValAlaLeuLeuGlyGluAsp
                                       AAGGAGGCGTACCAGAAGAGGAACAGCGTGCCGCTGGAGCGGGCCGTCGCGGGGGACACC
                                                                                          GATGAGAACTCCCTGACCAGGGTCATCACCACCGGCGTGAGGTGGACCTCAAACTGATT
                                                                                                           AspGluGlyAlaLeuThrArgIleValThrThrArgAlaGluIleAspLeuLysValIle
                                                                                                                                            ThrargProGluLeuTyrPheValAspValLeuArgSeralaIleAsnLysThrGlyThr
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